

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 124533

TO: Bao-Qun Li

Location: REM-3D24&3C18

Art Unit: 1648

Thursday, June 17, 2004

Case Serial Number: 09/899303

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Li,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

nucleic search, using sw model OM nucleic -

June 16, 2004, 08:32:08; Search time 1958.63 Seconds (without alignments) 14206.949 Million cell updates/sec

ou: Run

1 ATGCCCGGTTGCTCTTTCTC......TACTCTTTGCTCTAATAG 642 US-09-899-303A-3 Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6940544 Total number of hits satisfying chosen parameters:

3470272 segs, 21671516995 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database

gb_sts:* ggb_htg:, ggb_ov:, ggb_ov:, ggb_bat:, ggb_bi:,

gb_vi:* em_ba:* em_fun:* em_hum:* *:unem_in:*

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is the number of results predicted by chance to have a Š. Pred.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

B07544 Gene fragme B09288 CDNA encodi D00832 Hepatitis C E44260 CDNA encodi B04805 CDNA to 5'-B07391 CDNA encodi AB008441 Hepatitis AJ238800 Hepatitis D13558 Hepatitis C D10934 Hepatitis C AR207766 Hepatitis D50481 Hepatitis C AJ132996 Hepatitis AR165056 Hepatitis AR165055 Hepatitis D50485 Hepatitis C AX739971 Sequence AX238739 Hepatitis AR406040 Sequence AR406048 Sequence AR406050 Sequence AX036252 Sequence AX036258 Sequence AX794848 Sequence AAR157350 Sequence AX452736 Sequence AX452796 Sequence AX794890 Sequence AX774890 Sequence AX7748738 Sequence AX65050 Sequence AX65050 Sequence AB049101 Hepatitis AR157324 Sequence AX452752 Sequence AX685004 Sequence AX794846 Sequence AR157325 Sequence AX452754 Sequence AX685006 Sequence A48665 Sequence 3 A48667 Sequence 5 E04805 B07391 AB008441 HCJ238800 HPCJ483 HPCRNA AX739971 HCJ238799 AR406046 AR406046 HPCK1R2 HCV132996 AF165056 AF165055 HPCK1S2 AB049101 B07544 B09288 HPC5TRJ4 B04260 AX452752 AX685004 AX794846 AX794848 A48709 AX794890 A48711 AX452798 AX685050 AR157351 AX794892 14 DB 2082 2082 2082 2082 2082 2433 2433 2433 2433 9379 9410 9386 9386 9410 9598 3461 3461 1880 2540 2540 2540 3296 9033 Length 11076 11076 11076 11076 11076 Query 100.0 100.0 100.0 Score 619.8 619.8 619.8 619.8 619.8 619.8 619.8 619.8 619.8 575 573.4 575 578.6 578. 628.2 567 567 Result

ALIGNMENTS

PAT 07-MAR-1997

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DINA

A48665 642 bp Sequence 3 from Patent WO9604385. GI:2302378 unidentified unidentified unclassified. A48665 A48665.1 RESULT 1
A4865
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE ORGANISM REFERENCE AUTHORS TITLE

1 (bases 1 to 642)
Maertens,G., Bosman,F., De,M.G. and Buyse,M.
Maertens,G., Bosman,F., De,M.G. and Buyse,M.
PURIPIED HERATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND
THERAPENTIC USE
Patent: WO 9604385-A 3 15-FEB-1996; JOURNAL

PAT 17-OCT-2001

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Best Local Similarity 100.
Matches 642; Conservative
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         Other publication CA 2172273 960215
Other publication AU 3382495 960304
Location/Qualifiers
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Pred. No. 1.4e-150;
; Mismatches 0;
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AX452752
                                                                                                                                                                                                                                                                                                                                                                                           therapeutic use
Patent: 08-6245503-A.3.12-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned DNA"
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DEFINITION
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0; Mismatches 0;

    .639
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Hepatitis C virus
Viruses; BSRNA positive-strand viruses,
                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapeutic use
Patent: WO 02055548-A 3 18-JUL-2002:
INNOGENETICS N.V. (BE)
                                                                                                                                                                   AX685004 642 bp
Sequence 3 from Patent W002055548.
AX685004
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Best Local Similarity 100.0%;
Matches 642; Conservative (
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SOURCE
ORGANISM
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AUTHORS
TITLE
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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                                                                                                                                                     Maertens, G., Bosman, P., de Martynoff, G. and Buyse, M.A. Recombinant vectors for producing hov envelope proteins Patent: BP 1211315-A 3 05-JUN-2002; Innogenetics N.V. (8B)
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100.0%; Pred. No. 1.4e-150;
ive 0; Mismatches 0;
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1. .639
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                                                                                                                                                                                                                                                     Location/Qualifiers

    636
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    GI:21712437
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Best Local S:
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INNOCEMETICATION CA. 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
1..79="mailto:"mol_type="unassigned DNA" | Abstraf="taxon:32644" | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..792 | 1..79
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/mol_type="unassigned DNA"
/db_xref="taxon:11103"
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Patent: WO 03051912-A 3 26-JUN-2003;
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Sequence 3 from Patent WO03051912.
AX794846
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/protein_id="CAE48242.1"
/db_xref="G1:37515736"
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/note="unnamed protein product"
/codon start=1
/protein_id="Can18067.1"
/bote=in=id="Can18067.1"
/db_xref="Gi:21712440"
/db_xref="Gi:21712440"
/db_xref="Ci:21712440"
/db_xref="Ci:2171240"
/db_xref="Ci:2171
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Viruses; ssRNA positive-strand viruses, no DNA stage; Plaviviridae;
Hepacivirus.
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GCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA 241
                                                                       GCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCCACGCTCGCAGCTA
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/mol_type="unassigned DNA"
/db_xref="taxon:11103"
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                                                                  GGAACGCCACGGTCCCCACCACCACAATACGACGCACGTCGATTTGCTCGTTGGGGGCGG 301
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
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                                             CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCCACAAGCTGTCGTGGACATGGTGG
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Pred. No. 4e-147;
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Patent: US 6245503-A 5 12-JUN-2001;
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/mol_type="unassigned DNA"
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Sequence 5 from patent US 6245503.
AR157325 AR157325.1 GI:16218258
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/protein_id="Cad86520.1"
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/db xref="G1:2937141"
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Pred. No. 4e-147;
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                                  /note="unnamed protein product"
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Purified Hepatitis C Virus envelope proteins for diagnostic therapeutic use
Patent: WO 0205548-A 5 18-JUL-2002;
INNOGENETICS N.V. (BB)
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Macrtens, G., Bosman, F., De, M.G. and Buyse, M.
Macrtens, G., Bosman, F., De, M.G. and Buyse, M.
Macrtens, G., Bosman, F., De, M.G. and Buyse, M.
Macrtens, G., Bosman, F., De, M.G. and Buyse, M.
THERAPEUTIC USB
Patent: WO 9604385-A 47 15-FEB-1996;
INNOGENETICS NV (BB)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
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/note="unnamed protein product; Protein sequence is in conflict with the conceptual translation"
/codon_start=1
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Pred. No. 5.3e-145;
0; Mismatches 7;
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/db_xref="taxon:32644"
1. _2079
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Sequence 47 from Patent WO9604385.
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//b xxef="cf:37515738"
//translation="MAGKVIDTLTCGPADLVGYIPLVGAPLGGAARALAHGVRVLEDG
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GDLCGSVFLVSQLFT:1SPRHETVQDCNCS:1YGGHTTGHRMANDMMMNWSPTTALVVS
OLLRIPQAVVDWYAGAHWGVLAGLAYYSWVGNWAKVLIVMLLPAP.
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                                                                            Maertens, G., Depla, E. and Bosman, F.
Purified Hepatitis C virus envelope proteins for diagnostic and
therapeutic use
Patent: WO 93611912-A 5 26-JUN-2003;
INNOGENETICS N.V. (BB)
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/mol type="unassigned DNA"
/db_xref="taxon:11103"
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/note="unnamed protein product"
                       ssRNA positive-strand viruses,
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/db_xref="ef1:21712482"
/db_xref="ef1:2171248
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CIGCTTTCTGTTCCGCTATGTACGTGGGGACCTCTGCGGATCTGTCTTCCTCCTCCCCC
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Pred. No. 5.3e-145;
0; Mismatches 7;
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
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/mol_type="unassigned DNA"
/db_xref="taxon:11103"
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Sequence 47 from Patent BP1211315.
AX452796
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Matches 624; Conservative
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AR157350. GI:16218284
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Maertens, G., Bosman, F. and Buyse, M.A.
Purified Hepatitis C Virus envelope proteins for diagnostic
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    .2082
    /organism="Hepatitis C virus"
    /mol_type="unassigned DNA"
    /db_xref="taxon:11103"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAAGGTTTTGATTGTGATGCTACTCTTTGC 632
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Patent: WO 02055548-A 47 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Sequence 47 from Patent WO02055548.
AX685048
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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/procein_id="CAB48258.1"
/db_xref="G1:37515780"
/db_xref="G1:37515
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QLLRIPQAVVDMVAGAHWGVLAGLAYSMVGNWAKVLVVMLLFAGVDDHTRVGGGAAA
SDTGLVSLFSPESAQKTQLVNTNGSWHINRTPALCNDSLGTGFFAALFYRHFWSG
CPERLASCRSIDKFQGGGFLTYTBRNSSGDRYCWHYARPRCGIVPASGVGEPYVG
TPSPVVVGTTDRFGVPTYNWGANDSDVLILNNTRPPRGNTWFGCTWMNGTGFTXTCGGP
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FYRNMYVGOVERRERAACNWTRGBROLDERDRYSELSPLIATTENDLEVEFTLDP
ALSTGLIHHAONIVOYLYGOSAVVSLVIKWEYVLLLFILLADARICACLMMALLI
AQAEAALENLVVLNAAAVAGAHGTLSPLVFFCAAMYIKGRLVPGAAYAFYGWPLILLI
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                                                                                                                                                                                                                          Maertens, G., Depla, E. and Bosman, F.
Purified Hepatitis C virus envelope proteins for diagnostic
therapeutic use
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Pred. No. 5.3e-145;

    2079
    note="unnamed protein product"

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/mol_type="unassigned DNA"
/db_xref="taxon:11103"
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INNOGENETICS N.V. (BE)
Location/Qualifiers
1. .2082
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    .2076
    /product="unnamed"

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Search completed: June 16, 2004, 11:39:14 Job time : 1961.63 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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June 16, 2004, 07:39:53 ; Search time 241.553 Seconds Run on:

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US-09-899-303A-3

642 1 ATGCCCGGTTGCTCTTTCTC.....TACTCTTTGCTCTCTAATAG 642 Perfect score:

Seguence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* geneseqn1980s:* geneseqn1990s:* Database

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	11	Description
	}					1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
7	642	100.0	642	~	AAT12704	Aat12704 HCV B1
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m	642	100.0	642	σ	ADD55634	Add55634 Hepatit
4	628.2	97.9	795	N	AAT12705	S
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6	619.8	96.5	2086	~	AAT12973	Aat12973 HCV E1
10	619.8	96.5	2433	N	AAT12974	Aat12974 HCV E1
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12	8.809	94.8	2434	9	AAL48940	Aal48940 Hepatit
13	566.4	88.2	3461	~	AAQ64068	Aag64068 Non-A,
14	566.4	88.2	3461	N	AAT30386	Aat30386 5'UTR/C
15	565.4	88.1	1880	~	AAQ24467	Aag24467 NANB he
16	565.4	88.1	2187	~	ABA03491	Aba03491 Cuticle
17	565.4	88.1	2540	N	AAQ43889	Aaq43889 NANB he
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19	565.4	88.1	9605	9	ABK91431	Abk91431 Hepatit
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Abk91430 Hepatitis	Abk91428 Hepatitis	Abk91425 Hepatitis	Abk91426 Hepatitis	Abk91433 Hepatitis		Abk91427 Hepatitis	Aad25331 Hepatitis	Aaa98965 Hepatitis	Aaq15363 Pragment	Aaq26981 HCV gene	Aat03677 Hepatitis	Aaq80498 DNA encod	Aaq81559 Hepatitis	Aat03960 Partial H	_	Aal53723 Hepatitis	Aad49655 Hepatitis	Aaq29628 Hepatitis	Aaq25610 HCV in ex	Aaq22140 Hepatitis	Aaq20926 C10-E15 D
ABK91430	ABK91428	ABK91425	ABK91426	ABK91433	AAD25332	ABK91427	AAD25331	AAA98965	AAQ15363	AAQ26981	AAT03677	AAQ80498	AAQ81559	AAT03960	AAD25517	AAL53723	AAD49655	AAQ29628	AAQ25610	AAQ22140	AAQ20926
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88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	88.1	87.8	87.7	87.7	87.7	87.7	87.7	87.7	87.7	87.7	87.6	87.2	87.2	87.1
565.4	565.4	565.4	565.4	565.4	565.4	565.4	565.4	565.4	563.8	563.2	563.2	563.2	563.2	563.2	563.2	563.2	563.2	562.2	260	260	559
24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

AL IGNMENTS

AAT12704 standard; DNA; 642 BP. 23-SEP-1996 (first entry) HCV B1 construct HCCI9A. AAT12704; AAT12704

HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;

Hepatitis C virus.

WO9604385-A2.

15-PBB-1996.

95WO-EP003031. 31-JUL-1995; 94EP-00870132. 29-JUL-1994;

(INNO-) INNOGENETICS NV.

De Martynoff G, Buyse M; Bosman F, Maertens G,

WPI; 1996-129401/13.

Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.

Claim 23; Fig 21; 146pp; English.

tiss coordinate of the coordin

and B2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant B1, E2, and B1/B2 proteins. The ercombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or in reduction step with a disulphide constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more

Abk91411 Hepatitis

9605 6 ABK91411

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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines useful for inducing HCV specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for radsing antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence
                                                                                                                                                                                                                                                   New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein B1 or B2, useful for immunizing humans from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is a coding sequence described in the exemplification of the invention
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nes 642; Conservative 0
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                                                                        11-JAN-2002; 2002WO-EP000219
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                                                                                                                                                 (INNO-) INNOGENETICS
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serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and B1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human;
serotype; reversed phase hybridisation assay; genotype; antigen; sera;
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                                         TGCGTTCGGGAGAACAACTCTTCCCGCTGCTGGTAGCGCTCACCCCACCCCAGCGCT
                                                                                            AGGAACGCCAGCGTCCCCACCACCACAATACGACGCCACGTCGATTTGCTTCGTTGGGGGCC
                                                                                                                                                  GCTGCTCTCTGTTCCGCTATGTACGTGGGGGGATCTCTGGGGATCTGTCTCTCCTCGTCTCCC
                                                                                                                                                                                      CAGCTGTTCACCATCTCGCCTCGCCGCATCAGACGGTGCAGGACTGCAATTGCTCAATC
                                                                             AGGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCG
                                                                                                                                 GCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCC
                                                                                                                                                                                                     CAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACAGCGCAGGACTGCAATTGCTCAAATC
                                                                                                                                                                                                                                                      TATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGAACTGGTCGCCT
                                                                                                                                                                                                                                         TATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCT
                                                                                                                                                                                                                                                                                              ACAACGGCCCTGGTGGTATCGCAGCTGCTCCCGAATCCCAAGCTGTCGTGGACATGGTG
                                                                                                                                                                                                                                                                                                                      ACAACGCCCTGGTGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTG
                                                                                                                                                                                                                                                                                                                                                GCGGGGCCCCATTGGGGAGTCCTGGCGGCCTCGCCTACTATTCCATGGTGGGGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope prote in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                    GCTAAGGTTTTGATTGTGATGCTACTCTTTTGCTCTCTAATAG 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; Fig 21; 146pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV El or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV infected mammal. The present DNA sequence encodes an HCV El protein.
                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; vaccine; liver disease; B1 protein; B2 protein; liver fibrosis; ds; gene.
TATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCT
                                       ACAACGGCCCTGGTGGTATCGCAGCTCCCGGATCCCACAAGCTGTGGACGTGGACATGGTG
                                                                           GCGGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGG
                                                                                         GCGGGGCCCATTGGGGAGTCCTGGCGGCCTCGCCTATTCCATGGTGGGAACTGG
                          ACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCCACAAGCTGTCGTGGACATGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                              GCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG 642
                                                                                                                                              100.0%; Score 642; DB 9; L
100.0%; Pred. No. 2.2e-174;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                       Hepatitis C virus El protein coding sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 3; 271pp; English
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16-OCT-2002; 2002US-0418358P.
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P-PSDB; ADD55512.
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Hepatitis C virus clone HCCI10A B1 protein coding sequence

(first entry)

24-0CT-2002

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in vectors for the production of recombinant B1, B2, and B1/B2 proteins.

The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more in a sample, and in a serotyping assay for detecting one or more can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed B1, E2 and B1/B2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
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                                                                                                                                                                                                                                                                                                                             Score 628.2; DB 2;
Pred. No. 2.2e-170;
0; Mismatches 8;
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Best Local Similarity 98.89
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an El and an El protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunishing humans against HCV. The recombinant HCV El and/or El proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to in vitro monitoring sentence are pregnation. The present sequence is a coding sequence described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 161-162; 243pp; English.
                                                                                                              Hepatitis C virus; HCV; El protein; virucide; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buyse M;
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30-AUG-2001; 2001US-0315768P.
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AAL48914 standard; DNA; 795

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CTGCTTTCTGTTCCGCTATGTACGTGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV E1 or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present DNA sequence encodes an HCV E1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus, HCV, vaccine, liver disease, B1 protein, B2 protein,
                                       CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
                                                                                                                                                                                                                                          ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGAACTGGTCGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hepatitis C virus (HCV) vaccine composition, useful for reducing liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.9%; Score 628.2; DB 9; Length 795; Best Local Similarity 98.8%; Pred. No. 2.2e-170; Matches 633; Conservative 0; Mismatches 8; Indels 0
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16-OCT-2002; 2002US-0418358P.
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P-PSDB; AA018678.
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BP

standard; DNA; 2082

ADD55555

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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV lifection. The present sequence
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              New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans from
                                                                                                                                                                                                                                                                                                                           a coding sequence described in the exemplification of the invention
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Pred. No. 8.3e-168;
0; Mismatches 7;
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                                                                                               Example 2; Page 206-209; 243pp; English.
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                                                                                                                                                                                                             Hepatitis C virus, HCV, vaccine, liver disease, El protein, E2 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises an Hepatitis C virus (HCV) vaccine for reducin liver disease. The vaccine of the invention comprises an HCV El or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present DNA sequence encodes an HCV E1/R2 protein.
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liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal
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                                                                                                                                                          Hepatitis C virus E1/E2 protein coding sequence #13.
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Pred. No. 8.3e-168;
0; Mismatches 7;
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16-OCT-2002; 2002US-0418358P
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                                                                                                      (first entry)
                                                                                                                                                                                                                                               liver fibrosis; ds; gene.
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                         481
                                                                     541
                                                                                           694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins
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515 AGCTGTTCACCATCTCGCCTCGCCGATGAGACGGTGCAGGACTGCAATTGCTCAATCT 574
                                                                                                                                                                                                                                                                                                                                                  HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                      CAACGECCTGGTGGTATCGCAGCTCCGGATCCCACAAGCTGTGGTGGACATGGTGG
                                                                                                                                  CGGGGCCCATTGGGGAAGTCCTCGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGG
                                                                   CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
                                                                                                                 CGGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCTACTATTCCATGGTGGGGAACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope prote - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buyse M;
                                                                                                                                                                 CTAAGGTTTTGATTGTGATGCTACTCTTTGC 632
                                                                                                                                                                                CTAAGGTTTTGGTTGTGATGCTACTCTTTGC 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 23; Fig 21; 146pp; English.
                                                                                                                                                                                                                                                    AAT12973 standard; DNA; 2086 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCCGGCCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
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                                                                                                                                                                                                                                                                                                                                                                                GGAACGCCAGCGTCCCCACCACCACAATACGACGCCACGTCGATTTGCTCGTTCGGGCCGC
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                                                                                                  Gaps
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         Length 2086;
                                                                                                  Indels
Score 619.8; DB 2;
Pred. No. 8.3e-168;
0; Mismatches 7;
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         96.5%;
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                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  El construct HCCI66.
                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; vaccine; liver disease; El protein; E2 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCCCGGTTGCTCTTTCTCTATCTTTCCTCTTTACTGTCCTGTCTGACCATTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.5%; Score 619.8; DB 9; Length 2433; 98.9%; Pred. No. 8.8e-168; ive 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                             Hepatitis C virus E1/E2 protein coding sequence #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New hepatitis C virus (HCV) vaccine composition,
liver disease, e.g., liver fibrosis in a chronic
                                                                                       632
                                                                                                          CTAAGGTTTTGGTTGTGATGCTACTCTTTGC
                                                                                       CTAAGGITTTGATTGTGATGCTACTCTTTGC
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16-OCT-2002; 2002US-0418358P.
                                                                                                                                                                                                                   ADD55557 standard; DNA; 2433
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Matches 624; Conservative
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   liver fibrosis; ds; gene.
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P-PSDB; ADD55558.
                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
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                                                                                                                                                                                                                                                         ADD55557;
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                                                                                                                                        Purifying recombinant hepatitis C virus (HCV) El and E2 envelope prote in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 TGCCCGGTTGCTCTTTCTCTTCTCTTTGCTTTGCTGTCCTGACCGTTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                      Buyse M;
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                                                                    Martynoff
                                                                                                                                                                                                                   Claim 23; Fig 21; 146pp; English.
94EP-00870132
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nes 624; Conservative
                                    (INNO-) INNOGENETICS NV
                                                                      Bosman P,
                                                                                                      WPI; 1996-129401/13.
29-JUL-1994;
                                                                      Maertens G,
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             CGGGGGCCCATTGGGGAGTCCTGGCGGCCTCCCTACTATTCCATGGTGGGAACTGGG
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                                                                                   CTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTGCGGATCTGTCTTCCTCCC
                                                                                                            CTGCTTTCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGGATCTGTCTTCCTCGTCTCCCC
                                                                                                                                                         AGCITGITCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCT
                                                                                                                                                                           ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
                                                                                                                                                                                                                                                  CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
                                                                                                                                                                                                                                                                                                                       49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B2 protein; infection; gene;
ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus E2 protein related coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAAGGTTTTGATTGTGATGCTACTCTTTGC 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C virus; HCV; El protein; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВЪ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 2434
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P-PSDB; AA018679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are

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986 ACAACGCCCTGGTGGTATCGCAGCTGCTCCGACAAGCTGTCGTGGACATGGTG 1045
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useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                             Sequence 2434 BP; 434 A; 745 C; 714 G; 541 T; 0 U; 0 Other;
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1352 CAGGGGCCCACTGGGGAGTCCTGGCGGCCCTTGCCTACTATTCCATGGTGGGGAACTGGG 1411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant polypeptide comprising partial NSI region of hepatitis non-A non-B viral antigen - used in a method for detecting antibodies against hepatitis non-A non-B virus.
                                                         1112 AGCTGTTCACCTTCTCACCTGGCGGTATGAGACGGTACAGGACTGCAACTGCTCAATCT
                                           422 ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
                                                                                               482 CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTGGTGGACATGGTGG
                                                                                                                                                        542 CGGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; antigen; detection; antibody; ds.
                                                                                                                                                                                                                           1412 CTAAGGTCTTGATTGTGATGCTACTCTTTGCT 1443
                                                                                                                                                                                                            602 CTAAGGITTTGATTGTGATGCTACTCTTTGCT 633
                                                                                                                                                                                                                                                                                                                                                                                                             5'UTR/CORB/ENV/NS1/NS2/NS3 cDNA from HCV (#4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/product= "Core peptide"
880. .1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "NS2 and NS3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 10-12; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "NS1/ENV2"
2737. 3461
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307. .3461
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/product= "ENV1"
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307. .879
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P-PSDB; AAR98361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus.
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22-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus #4 and #6 genes were isolated (AAQ64068-69). Both genes contain the core, ENV, NS1, NS2 and NS3 regions. A core region fragment is given in AAQ64067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA coding a Non-A.Non-B hepatitis virus antigen - useful for detecting HCV within serum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCCGCTTATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACAAACGACTGCTCCA
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88.2%; Score 566.4; DB 2; Length 3461;
Best Local Similarity 93.5%; Pred. No. 2.3e-152;
Matches 591; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3461 BP; 638 A; 1046 C; 1012 G; 765 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                   (TOFK) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
(SANW ) SANWA KAGAKU KENKYUSHO CO.
(TOFU ) TONEN CORP.
                                                                                                                                                                                                                            'note= "NS3 N-terminal"
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                    location/Qualifiers
                                                                       /*tag= b
//abal= core
//abal= core
//abal= ENV
//atag= ENV
//atag= d
//abal= NS1
2737. 3461
//tag= NS23
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P-PSDB; AARS4066.
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amino acids 384-495 of the HCV NS1 antigen. These protein fragments may be used in the detection of antibodies against HCV. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                     AGCTGTTCACCTTCACCTCGCCGGTATGAGACGGTACAGGACTGCAACTGCTAATCT
                                                                                                                                                                         CTTCCGCTTATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACAAACGACTGCTCCA
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                                               Sequence 3461 BP; 638 A; 1046 C; 1012 G; 765 T; 0 U; 0 Other;
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                                                                       Score 566.4; DB 2;
Pred. No. 2.3e-152;
0; Mismatches 41;
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Matches 591; Conservative
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non-A, non-B hepatitis virus; NANBHV; PCR; amplification polymerase chain reaction; vaccine; antibody; ss. hepatitis virus strain HC-J4 genome Location/Qualifiers 342. .1880 BP AAQ24467 standard; DNA; 1880 (first entry) Non-A. non-B hepatitis virus. 09-NOV-1992 NAMB

This sequence is the genome of the non-A, non-B hepatitis virus (NANBHV) strain HC-J4. This sequence was derived by amplification by polymerase chain reaction. The nucleotide sequences derived from this amplification can be used to detect NANBHY infection which could not be detected by conventional methods. The detection kits allow highly specific and sensitive detection at an early phase of infection. The polypeptide product of this coding sequence can be used for the manufacture of vaccines and immunological pharmaceuticals and also to produce antibodies Recombinant cDNA of NAMBH virus strain HC-J5 and corresp. peptides -useful for diagnosis and in vaccines and immunological pharmaceuticals. Sequence 1880 BP; 333 A; 593 C; 556 G; 398 T; 0 U; 0 Other; Disclosure; Page 11; 42pp; English. а НС-J4 91EP-00310297 90JP-00304405 /*tag= ¿ /label= I (IMMO) IMMUNO JAPAN INC. Okamoto H, Nakamura T; WPI; 1992-160959/20. P-PSDB; AAR24087. specific to NANBHV 07-NOV-1991; 08-NOV-1990; 13-MAY-1992 BP485209-A.

Gapa ó, Length 1880; Indels Score 565.4; DB 2; Pred. No. 3.6e-152; 0; Mismatches 41; Query Match
Best Local Similarity 93.5%;
Matches 590; Conservative 0

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1026 1086 1146 906 121 996 181 241 361 1027 GCGITCGGGAGGACAACAGCTCCCGTIGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCCA 302 CTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTCGGGGATCTGTCTTCCTCGTCTCCCCC 182 GCGTTCGGGAGAACAACTCTTCCCGCTGCTGGTAGCGCTCACCCCCACCCTCGCAGCTA 242 GGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGGG 1087 62 윱 셤 셤 셤 셤 δ Š ð ò ठ

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CAACGCCCTGGTGGTATCGCAGCTGCTCCCGCATCCCACAAGCTGTGGTGGACATGGTGG

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Perfect score:

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Run on:

Scoring table:

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CA916001 CA12E1301
AV63601 AV631821
AV637507 AV637507
AV637983 AV637983
AV637328 AV637328
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AV630153 AV63013
AV630154 AV63013
CA659369 wlml.pk00
AL101589 Drosophil
BB337089 894043G08
BL73733 1031067F0
BJ536011 BJ536071
BX356664 BX356664
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CC605275 OGUHI31TH
BES78381 m8A2_5817
CG286130 OGXBF16TV
BZ555011 pacs1-60_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens cDNA BM clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Pax: 86-21-50801922
Bmail: hansg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV755731 AW Homo sapiens CDNA clone BMFAKB03 5', mRNA sequence.
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                                                          BJ536071
BX356664
AA459034
CA816001
BI723734
AV637507
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AV638125
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VERSION
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AV758366 AV758366
CF846043 psHB036xB
AL053013 Drosophil
                                                                                              16, 2004, 09:12:53 ; Search time 1725.91 Seconds (without alignments) 11108.065 Million cell updates/sec
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1 ATGCCCGGTTGCTCTTTCTC.....TACTCTTTGCTCTCTAATAG
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                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                        27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         nucleic search, using sw model
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DB seq length: 200000000
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[1] [bases I to 492]
[30, J., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Eng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Ru, G., Ren, S., Zhong, M., Chen, Z., Zhong, M., Chen, Z., Zhong, M., Chen, Z., Zhang, Q., Chen, S., Han, Z. and Chen, Z.
                                                                                                                                                                                                                                                                                                                                                                      292 GTTGGGGCGGCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTC 351
                                                                                                                                                                                                                                                                                                                   472 GTGGTGTCACACTCGCTCTGCTCAGCTCTTACGTGTGGGACCTCTGCGACGGAGTGATG 413
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Unpublished (2000)
Unpublished (2000)
Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801919(ex.45)
Email: hanzgechggc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                          /tissue_type="Bone marrow"
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/lab_mole="BM25.8"
/clone_lib="BM"
/note="Vector: pTriplBx2; Site_1: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV758366 BM Homo sapiens cDNA clone BMFAKA03 5', mRNA sequence.
AV758366
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/mol_type="mRNA"
                               organism="Homo sapiens"
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ocation/Qualifiers
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AV758366/c
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CP846043 534 bp mRNA linear BST 30-OCT-2003 psHB036xB09f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sHB Phytophthora sojae cDNA clone sHB036B09 5, mRNA sequence.
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                                                                                                                       /clone_lib="BM"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 ---ATTATCTCTGGGGGGGAACHTGTTTGTGGAAGAATGCAACTGCTCATTCTATCCT
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                                                 /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
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Phytophthora sojae
Bukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
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14.4%; Score 92.6; DB 9; Length 4
Best Local Similarity 61.1%; Pred. No. 7.2e-12;
Matches 185; Conservative 0; Mismatches 114; Indels
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Tel: 540-231-7318
Email: bmtyler@vt.edu
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/organism="Phytophthora sojae"
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/db xref="taxon:67593"
/clone="sHB036B09"
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'db_xref="taxon:9606"
                           clone="BMFAKA03"
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Unpublished (2003)
Contact: Tyler B
Tyler lab
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/tissue_type="mycelium"

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/mol_type="mRNA"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
Br 191 91006 BWYR cedex - FRANCE (B-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutcyo Oscogawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
BCORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
Pl and BST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACK19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                           70 TATGAGGTGCGCAACGTGTCCGGGATGTACCATGTCACGACGACTGCTCCAACTCAAGC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 AACTICCIGACGACGACGACGTCTCGCAGGIATACGICATCGGCGCGGAGACGGCACCCAC 439
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genes during infection and propagation_sHB"
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                Query Match 6.5%; Score 41.6; DB 14; Length 534;
Best Local Similarity 47.1%; Pred. No. 20;
                                                                                                                                                                                                                      Pred. No. 20;
0; Mismatches 144; Indels
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 cerececcaacaacarcresaacacreece 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 TGTTCCGCTATGTACGTGGGGGATCTCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence.
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                                                                                                                                                                                                                                            Matches 128; Conservative
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LADSDASBY 590 bp MRNA linear BST 24-NOV-2002 wlml.pk0005.c9 wlml Triticum aestivum cDNA clone wlml.pk0005.c9 5' end, mRNA sequence.
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                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                     182 GOGITCGGGAGAACACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 KCSSTSBSCSCCCSSKSVCGTSCSS----SSSCSSSSTSSSTSKSSSGSSSS 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 CTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   665 SSSSYTTSKSTSASGSGSWSAGGGSGSTGSTSSSSSSSTSTSSSSVSSGSKSSTBSSGS 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 AGCTGTTCACCATCTCGCCTCGCCGCATGAGACGGTGCAGGACTGCAATTGCTCAATCT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 SGSSSSSVGTSSSSDSTSTCCSCCCYMCTCCSTYBMBCYTSTSCGGSSSSSGKGGVTKCG 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

1 (bases 1 to 590)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.

Dubont Wheat cDNA Sequence
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                     242 GGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTTGCTCGTTGGGGCGG
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Scott V. Tingey
Crop Genetics
B. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DB 19714-6104, USA
Far: 302-631-2607
Email: Scott.V. Tingey@USA.dupont.com
                                                                                                                                                                                         4
                                                                                                                                           Length 925;
                                                                                                                                                                                         Indels
                                                                                                                                                                                         69; Conservative 165; Mismatches 198;
                                                                                                                                         DB 29;
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                                                                                                                                                                  45;
                                                                                                                                         Score 40.6;
                                                                                                                                                                  Pred. No.
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/db xref="taxon:7227"
                 /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                         6.3%;
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Anote="Vector: pBluescript II SK-; Site_I: BCORI; Site_2: XhOI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (actate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. POlyA mRNA was purified from each sample, pooled and CDNA synthesized. The CDNA was directionally cloned into lambda ZAP II (Stratagene) in the ECORI (5') and XhOI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with EXASsist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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| grain="CC-1690 wild type mt+ 21gr"
| db xref="taxon:3055"
| clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB337089 525 bp mRNA linear BST 14-JUL-2000
894043G08.yl C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                      CCTCGTCTCCCAGCTGTTCACCATCTCGCCTGCCATGAGACGGTGCAGGACTGCAA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 TINTSNSTSSNNSATGSSSSNSSGGGTTBSGSSSSSSSNNNNNNAKASNNSBTSNSNN 370
                                                                                                                                                                                                                                                                                                            411 TIGCTCAATCIATCCCGGCCACATAACAGGTCACCGIATGGCTTGGGATATGATGATGAA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 SNSATTSSTNGSSGSSSSSSSSSSSSTSSNTSTSSTSNSSNSNTSSTTSSSSTTNSTSTSSS 430
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Chlamydomonas reinhardtii
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomenas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants, project phase 2
                                                                                                                                                                                                                                                                                                                                                                   191 SCCCSNCTRCRNRNTTNTTNSSSSSSNSNNNTRNRNNSNNNSNNNSSNNNSSSSSSSNNNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471 CTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCAAAGCTGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 GGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGT
; Score 40.4; DB 29; Length
; Pred. No. 43;
85; Mismatches 144; Indels

    . 525
    /organism="Chlamydomonae reinhardtii"

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Contact: Blizabeth H. Harris
DCMB Box 91000
Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Tel: 919 613 8164
Pax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591 GGGGAACTGGGCTAAGG 607
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    Query Match 6.3%
Best Local Similarity 10.9%
Matches 28; Conservative
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogater BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBelobacieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 26-JUL-1999
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 GGACATGATCATGCACACCCCCGGGTGCGTGCCTTGCGGAGGAACAACTCTTCCCG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 CTCC6TGCGCGCGCGCCTGGGACGGCCCCTCTCCTCGGCGCGCCTCATCATGCAGGGCCG 282
/db xref="taxon:4565"
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/tissue type="leaf"
/clone lib="wlm1"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) seedlings 1 hr after inoculation with Erysiphe graminis f. sp tritici"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS01213 Francisco CNS01213 Francisco CNS01213 Drosophila melanogaster genome survey sequence T7 end of BAC BACN08C07 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                   Length 590;
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                                                                                                                                                                                                                                                                                                                                                              Query Match 6.3%; Score 40.4; DB 14;
Best Local Similarity 47.3%; Pred. No. 42;
Matches 122; Conservative 0; Mismatches 136;
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Drosophila melanogaster
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/mol type="genomic DNA"
/db xref="taxon.7227"
/clone="BACNO8C07"
/clone lib="DrosBAC"
/plasmid="pB-DBACI1"
/note="end : T7"
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CNS01213

RESULT 6

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TITLE JOURNAL AUTHORS REFERENCE

COMMENT

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BJ536071 MF01SSB CDNA Oryzias latipes CDNA clone MF01SSB002D03 3',
                                                                                                                                                                                                                                                                                                                                               108 GAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryzias latipes (Japanese medaka)
Oryzias latipes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterrygii, Neopterrygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterrygii; Percomorpha; Atherinomorpha;
Belonicormes; Adrianichthyidae; Oryzinae; Oryzias.
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Medaka EST Project in Takeda's lab
Unpublished (2001)
lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                              Gaps
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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/clone_lib="MF01SSB cDNA"
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52.1%; Pred. No. 58;
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/clone="MF01SSB002D03"
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Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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/strain="Hd-rR"
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                                                                                                                                                                                                                                                                              Matches 124; Conservative
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Chlamydomonas reihhardtii
Bukaryota; Viridiplantes; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Grossman, A., Chang, C.-W., Davies, J., Harris, B., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
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1031067F08.yl C. reinhardtii CC-1690, Stress II (normalized)
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA seguence
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/strain="CC-1690 wild type mt+ 21gr"
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Unpublished (2001)
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DCMB Box 91000
Duke University
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                                                                                                            Best Local Similarity 47.0
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Fax: 919 613 8177
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                                                                  821 SSTTISTKSBBITTISBBIBSSSTSSTWITBISCTSSTINITISSYSSBSTSBBITSSTTS 880
                                                                                                                                     369 CACCATCTCGCCTCGCCGCATGAGACGCTGCAGGACTGCAATTGCTCAATCTATCCCGG 428
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765 STTBYTBSSSYBSBSS----BTTSSCSCTSSBSTTSSTBSMTSSSBTCTSSSSSSSBTT 820
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bmail: cgapbe-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 382.
                                                                                                                                                           CTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTT
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/db_xref="GDB:6032522"
/db_xref="taxon:9606"
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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Best Local Similarity
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                                                                                                                                     487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organisma="Homo sapiens"
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/clone lib="Fund cloned with a NotI-oligo dIT)
/primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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  446 GTATGGCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGTATCGCAGC 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
1 (Liw.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bra 191 91006 EVRX cedex - Prance
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIOISCAOZNP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      645 TSNTTTBTBTTSSSSTSSSTTSSSTTSSSSTSSSSSBBTTTSSSTSSSSTTSS
                                          606 GTACGGCTTNGGCTGCGAGGACTCCCTCAACCACCTGAATTATGTGGCCCCAACG
                                                                                        506 TGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCCATTGGGGAGTCCTGG
                                                                                                                                     546 TCTTTGAGACCTCGCCACATGTCATGCGCGGTGATGGGGGCCCTGGAGGGTCTCCGGG
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Best Local Similarity 13.6%; Pred. No. 71;
Matches 77; Conservative 223; Mismatches 264; Indels
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/clome lib="Cabernet Sauvignon Leaf - CA12EI"
/clome lib="Cabernet Sauvignon Leaf. Sfil; Site_2:
Sfil; CA12EI is a cDNA library of Cabernet Sauvignon
leaves. The leaves were collected on July 25, 2001, in
Napa Valley, California, and represent leaves in
mid-season development. These leaves were verified to be
infected with the bacterial pathogen, Xylella fastidiosa,
based on a diagnostic assay using PCR and Xylella-specific
primer pairs. The plants were asymptomatic at the time of
collection, but later developed symptoms. CDNAs were made
by oligo-dT priming and directionally cloned. 5'and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGTGGCCATTACGGCGGG-3' and
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA816001
CA12E1301IVF B04 Cabernet Sauvignon Leaf - CA12E1 Vitis vinifera CDNA clone CA12E1301IVF_E04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vitis vinifera
Vitis vinifera
Vitis vinifera

Straptophyta; Embryophyta; Tracheophyta;

Bukaryota; Vitidiplantae; Straptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; Vitaceae; Vitis.

I bases I to 621,

Goes da Silva, F. Lim, H., Iandolino, A., Baek, J., Jones, K.,

Walker, M.A. and Cook, D.R.

Transcriptional responses of Vitis vinifera to infection by the bacteries.
                                              195 CAACTICTICCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGT 254
                                                                                            CCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTCTCTGTTC 314
                                                                                                                                                                                           143 cécrhécécercesecercégésececraricarientes resecretarientes 202
                                                                                                                                                                                                                                           315 CGCTATGTACGTGGGGGATCTTCTGCGGATCTGTCTCCTCGTCTCCCAGCTGTTCACCAT 374
                                                                                                                                                                                                                                                                                            203 CATCAGGGAGCAGCGTGACTTCAGCGAGTCCCGCGAGCACCTGGCTAGACAGGTTAACAAG 262
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                                                                                                                                                                                                                                                                                                                                             375 CTCGCCTCGCCGGCATGAGACGGTGCAACTGCAATTGCTCAATCTATCCCGGCCAC 432
                                                                                                                                                                                                                                                                                                                                                                    263 CACGTCCTTCCAGCCTGAGCCAGCAGGTTTGGGAAGGGGCTTCCTGGCCCCCCCAC 320
     Gaps
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  Indels
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/mol type="mRNA"
/cullivar="cabernet Sauvignon"
/db xref="taxon:29760"
/clone="CA1281301UP_E04"
/sex="hermaphrodite"
/dev stage="Wid-season leaf material"
/lab_host="DH5alpha"
  0; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Doug Cook
CARS Genome Facility
UC Davis Department of Plant Pathology
1 Shields Ave., Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bmail: drcook@ucdavis.edu
Seq primer: GTTATCAGTCGACGGTACC.
Location/Qualifiers
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Matches 114; Conservative
                                                                                                                                               255
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CA816001
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ORIGIN

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/db xref="taxon:3055"
/dlone_lib="C. reinhardtii CC-1690, Stress II
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/note="Vector: pallabescript II SK-; Site_1: BCORI; Site_2:
XhOI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr); H2 production
conditions (0, 12hr, 24hr); TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the BCORI (5) and XhORI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B1723734 1031067F08.y2 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                 111 CGACTGCTCCAACTCAAGCAITGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGG 170
                                                                                                                                                                                                                       397 caactrorecrrerearecaageeraageeraageacaageageageagererecaagererecaag 456
                                                                                                                                                                                                                                                                                                  171 GTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCAC 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 GCTCGCAGCTAGGAACGCCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          517 ACACTTCGGTGGTTTCGGCAGCGTAGCCGCTGACACCATCGGAAGCATAGCTGGTGGTCGG 576
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Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Crossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shraqer, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Onicellular System for Analyzing Gene Function and Regulation in
Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
                                                                              Gaps
                                                                              ö
       Length 621;
                                                                              Indels
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/strain="CC-1690 wild type mt+ 21gr"
                                                                          95;
DB 14;
   Query Match
6.1%; Score 39; DB
Best Local Similarity 50.3%; Pred. No. 94;
Matches 96; Conservative 0; Mismatches
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Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
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Chlamydomonas reinhardtii
ISM Chlamydomonas reinhardtii
Bukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
Chlamydomonadaceae; Chlamydomonas.

Asamizu, B., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
daneration of expressed sequence tags from low-CO2 and high-CO2
IL DNA Res. 7 (5), 305-307 (2000)

M. 20539644

ID 1089912

Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Bmail: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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/clone="HC074a01_r"
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/note="Vector: pBluescriptII SK.; Site 1: BcoRI; Site 2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV637507 Av637507 434 bp mRNA linear BST 15-DEC-2000 AV637507 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
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/mol type="mRNA"
/strain="C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA clone HC074a01_r 5', mRNA sequence. AV637507.1 GI:10780827
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Matches 92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV638521 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii cDNA clone HC087407_x 5', mRNA sequence.
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Asamizu, E., Miura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonas reinhardtii
Bukaryota, Viridiplantes; Chlorophyta, Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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                                                     Length 624;
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Pred. No. 94;
0; Mismatches 141; Indels
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/mol_type="mRNA"
/strain="C9"
/db_xref="raxon:3055"
/clone="HC087407_r"
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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GenCore version 5.1.6
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US-08-11-160-21
                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                             682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            - nucleic search, using sw model
                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                               US-09-899-303A-3
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Match Length
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                                                                                                                          Perfect score:
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                                                                 Run on:
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Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 27, Appl	Sequence 21, Appl	Sequence 21, Appl
US-08-384-616-3	US-08-904-686A-3	US-09-315-850-3	US-08-324-977-11	US-08-384-616-11	US-08-904-686A-11	US-09-315-850-11	US-08-324-977-13	US-08-384-616-13	US-08-904-686A-13	US-09-315-850-13	US-08-324-977-1	US-08-384-616-1	US-08-904-686A-1	US-09-315-850-1	US-08-823-895A-27	US-08-086-428B-21	US-08-468-570-21
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28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: MAERTENS, GERRT
APPLICANT: BOSMAN, PONS
APPLICANT: BOSMAN, PONS
APPLICANT: DE MARTYNOPP, GUS
APPLICANT: DE MARTYNOPP, GUS
TITLE OF INVENTION: PORIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS POR DIAGNOSTIC AND THERAPEUTIC USE
TOTRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                            STREET: 11100 FOLLOWARD STREET: 11100 FOLLOWARD STATE: VIRGINIA STATE: PLOPPY disk COMPUTER READABLE FORM: PC-DOS/MS-DOS OPERATING SYSTEM FOLLOWS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 (RPO) CURRENT APPLICATION NUMBER: US/08/612,973 FILING DATE: 11-MAR-1996 CLASSIFICATION THANER: 32.205 REGISTRATION MOMBER: 32.205 REGISTRATION NUMBER: 32.205 REGISTRATION NUMBER: 1467-10 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4100 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4100 STELEPHONE: (703) 816-4100 STELEPHONE: (703) 816-4100 STELEPHONE: SAGUENCE CHARACTERISTICS: TEMPTHER: 642 Dase palie
                            Sequence 3, Application US/08612973; Patent No. 6150334
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TYPE: nucleic acid
STRANDEDNESS: single
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                       US-08-612-973-3
RESULT 1
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Sequence Sequence Sequence

-08-150-204E-96

Sequence Sequence Sequence

Sequence

-08-904-686A-9

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241 AGGAACGCCACGCCCCCCCCCCCCACCACATACGACGCCACGTCGATTTGCTCGTTCGGGGG 300
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          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                   ALTLING DATE:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
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                                                                                                                                                                                                                                                                                             LENGTH: 642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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NAME/KEY:
LOCATION:
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, LOCATION:
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Batent No. 6245503

GENERAL INFORMATION:
APPLICANT: BASHAN, FONS
APPLICANT: BOSHAN, FONS
TITLE OF INVENTION: PROTEINE HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
OVERESPONDENCE ADDRESS:
ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ALINGTON
STREET: 1104 NORTH GLEBE ROAD
CITY: ALINGTON
STREET: 1200-14714
                                                               Gaps
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0
                                Length 642;
                                                              0; Indels
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                             Query Match 100.0%; Score 642; DB 3; L
Best Local Similarity 100.0%; Pred. No. 4.5e-161;
Matches 642; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
US-08-612-973-3
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                                                                                       GCGTTCGGGAGAACAACTCTTCCCGCTGCGTAGCGCTCACCCCCCACGCTCGCAGCTA
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    GENERAL INFORMATION:
APPLICANT: MAERTENS, GERRT
APPLICANT: BCANN, FONS
APPLICANT: BCANN, FONS
APPLICANT: BUXER, MARINEP, GUY
APPLICANT: BUXER, MARINEP, GUY
APPLICANT: BUXER, MARINE-ANGE
TITLE OF INVENTION: POURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATKON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON WORTH GIBEB KOAD CITY: ARLINGTON STATE: VIRGINIA COURTY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: RIDPPY disk
COMPUTER: ISM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
RILING DATE:
CLASSIPTCATION:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS B.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKT NUMBER: 1487-10
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     755 CTAAGGITTTGATTGTGATGCTACTCTTTGCTCCCCTAATAG 795
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; Sequence 5, Application US/08927597
; Patent No. 6245503
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GCGGGGCCCATTGGGGAGTCCTGGCGGCCTCGCCTACTATTCCATGGTGGGGAACTGG 600
                      155 TGCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCCTGACCGTTCCAG 214
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                                                                                                                                                                                                                         Sequence 5, Application US/08612973
Fatent No. 6150134
GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
APPLICANT: BUXSM, MARTYNOFF, GUY
APPLICANT: BUYSB, MARTS-ANGE
TITLE OF INVENTION: PUBLFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PURFIES FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
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                                                                                       642
                                                                                                         601 GCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR.1996
CLASSIFICATION: 435
                                                                                       GCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTATION NUMBER: 32.205
REFERENCE DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: NIXON & VANDERHYB P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
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FEATURE:
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, LOCATION:
US-08-612-973-5
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US-08-612-973-5
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                APPLICANT: BOSMAN, FONS
APPLICANT: DB MARTYNOFP, GUY
APPLICANT: BUYES, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CARRESPONDENCE ADDRESS:
ADDRESSEB: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                           STATE: VARGAGE COUNTRY: U.S.A.

ZIP: 22201-473.

ZIP: 22201-473.

ZIP: 22201-474.

COMPUTER READALE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPACIBLE
OWENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION DATE: II-MAR-1996
CURRENT APPLICATION DATE: II-MAR-1996
FILING DATE: II-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION UNDER: 1487-10
TELEFAN: (703) 816-4100
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
ILENGTH: 2082 base pairs
TTENDER: MICHER STATE
THOME: ATTORNEY CHARACTERISTICS:
LENGTH: 2082 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 98.9
Matches 624; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: mucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                         VIRGINIA
                                                                                                                                                                     CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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FEATURE:
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TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INPOMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: ODA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                           mat_peptide
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                                                                                                                                                                     ANTI-SENSE: NO FEMTURE:
                                                                                                                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
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US-08-927-597-5
                                                                                                                                                                                                                                                        NAME/KEY:
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US-08-612-973-47
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Sequence 47, Application US/08612973 Patent No. 6150134 GENERAL INFORMATION:

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Best Local Similarity 98.9
Matches 624; Conservative
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-927-597-47
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US-08-612-973-49
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 CTGCTTTCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCC 514
                                                                                                                                                                                                                                                      CGGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGG 601
                                                                                                                         AGCTGTTCACCATCTCGCCTCGCCGCCATGAGACGGTGCAGGACTGCAATTCCTCAATCT
                                                                                                                                                                             CAACGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG
                                     AGCTGTTCACCATCTCGCCTCGCCGCATGAGACGGTGCAGGACTGCAATTGCTCAATCT
                                                                                                          ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MAERTENS, GERRT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GT
APPLICANT: DE MARTYNOFF, GT
APPLICANT: BUYSE, MARTIS-ANGE
TITLE OF INVENTION: PROTBINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF SEQUENCES: 111
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/927,597 FILING DATE:
                                                                                                                                                                                                                                                                                                                            632
                                                                                                                                                                                                                                                                                                                                               CTAAGGTTTTGGTTGTGATGCTACTCTTTGC 785
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CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-WAR-1996
ATTORNEY/AGENT INPORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 1487-10
FELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 816-4100
TELEPAK: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPALIBLE
COMPUTER: IRM PC COMPALIBLE
COMPUTER: IRM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 47, Application US/08927597; Patent No. 6245503; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
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ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 GCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 GCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGGTA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 AGCTGTTCACCATCTCGCCTCGCCATGAGACGGTGCAGGACTGCCAATTGCTCAATCT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGG
                                                                                                                                    275 ACTCAAGCATTGTGTATAGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCTGCCCT
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                                                                                                        2 TGCCCGGTTGCTCTTTCTCTTTCTCTTTGGCTTTACTGTCCTGTCTGACCATTCCAG
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                                                       Gaps
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APPLICANT: MARKTENS, GERRT
APPLICANT: BOSMAN, POOP
APPLICANT: BOSMAN, POOP
APPLICANT: BUSSE, MARTHOFF, GUY
APPLICANT: BUSSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                       ..
96.5%; Score 619.8; DB 3; Length 2082; 98.9%; Pred. No. 4.7e-155; ive 0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                               US-08-927-597-49

Sequence 49, Application US/08927597

Sequence 49, Application US/08927597

Patent No. 6445503

GRNERAL INFORMATION:
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUSMAN, FONS
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS POR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy Alsk
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
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Pred. No. 4.9e-155;
                                                                                                                                                                      1106 craaccirriccircrearccracicriric 1136
                                                                                                                  602 CTAAGGITITGAITGIGAIGCIACICTITGC 632
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CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
... LENGTH: 2433 base pairs
... ERVETH: ALLES ALLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B: NIXON & VANDERHYB P.C.
1100 NORTH GLEBE ROAD
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98.9%;
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Best Local Similarity 98.9
Matches 624; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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MOLECULE TYPE: cI
HYPOTHETICAL: NO
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FEATURE:
NAME/KEY: CDS
LOCATION: 1..2
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US-08-927-597-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 TGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGCTTTTGCTGTCCTGACGTTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.5%; Score 619.8; DB 3; Length 2433; 98.9%; Pred. No. 4.9e-155; ive 0; Mismatches 7; Indels 0;
               MEDIUM TYPE: FLORY:
MEDIUM TYPE: TBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SPERATIN SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (RPO)
SOFTWARE: PATENTIN ROYON BATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E:
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 36,400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
TYPE: mucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 96.5
Best Local Similarity 98.9
Matches 624; Conservative
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   COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY:
, LOCATION:
US-08-612-973-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGGGGCGTGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTCTCTGCTCCGCTATGTACGTGGGAATCTCTCTGCGGATCTGTTTTCCTCGTCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCAGCCCTAGTGGTATCGCAGTTACTCCGGATCCCACAAGCTGTCGTGGTAGTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2498 GCGTTCGGGAGAACAACTCCTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCCA
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       NAMB/KEY: CDS
LOCATION: (1813)..(10845)
OTHER INFORMATION: hepatitis C virus polyprotein from core to OTHER INFORMATION: nonstructural protein NS5B; parental sequence OTHER INFORMATION: without cell culture-adaptive mutations
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Pred. No. 1.9e-140;
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TITLE OF INVENTION: Hepatitis C Virus Cell Cultus
FILE REPERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT PILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.5%;
Matches 590; Conservative
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NAME/KEY: 3'UTR
; LOCATION: (10846)..(11076)
US-09-539-601-1
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APPLICANT: Bartenschlager, Ralf FW
TITLB OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT APPLICATION NUMBER: 199 15 178.4 GERWANY
EARLIER APPLICATION NUMBER: 199 15 178.4 GERWANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
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NAME/KSY: 5.UTR
LOCATION: (1)..(341)
OTHER INFORMATION: construct 1389/Core-3'/wt
FEATURE:
NAME/KSY: CONSTRUCT
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NAMB/KEY: RBS
LOCATION: (1202)..(1812)
OTHER INFORMATION: internal ribosome entry site from OTHER INFORMATION: encephalomyocarditis virus
FRATURE:
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ORGANISM: Hepatitis C virus
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, LOCATION: (10846)..(11076)
US-09-539-601-25
                                                                                                                                       GENERAL INFORMATION:
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NAME/KEY: CDS
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NAME/KRY: RBS

LOCATION: (1202)...(1812)

OTHER INFORMATION: internal ribosome entry site from

OTHER INFORMATION: encephalomyocarditis virus

FEATURE:

NAME/KRY: CDS

LOCATION: (1813)...(10845)

OTHER INFORMATION: hepatitis C virus polyprotein from core to

OTHER INFORMATION: nonstructural protein NSSB; carries cell

OTHER INFORMATION: culture-adaptive mutations from clone 9-13F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indele
                                                                                                                     FRATURE:
NAME/KGY: CDS
LOCATION: (132)..(1193)
OTHER INFORMATION: hepatitis C virus core - neomycin
OTHER INFORMATION: phosphotransferase fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 88.1%; Score 565.4; DB 4;
Best Local Similarity 93.5%; Pred. No. 1.9e-140;
Matches 590; Conservative 0; Mismatches 41;
                                                                                           LOCATION: (1)..(341)
OTHER INFORMATION: construct 1389/Core-3'/9-13F
                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: 3'UTR
; LOCATION: (10846)..(11076)
US-09-539-601-19
                               TYPE: DNA
ORGANISM: Hepatitis C
                                                                           NAME/KEY: 5'UTR
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OTHER INPORMATION: hepartitis C virus polyprotein from core of the INFORMATION: nonstructural protein NS5B; carries cell OTHER INFORMATION: culture-adaptive mutations of clone 5.1
                                                                                                                                                                                                                                                                   Culture System
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OTHER INFORMATION: hepatitis C virus core - neomycin
OTHER INFORMATION: phosphotransferase fusion protein
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OTHER INFORMATION: internal ribosome entry site from OTHER INFORMATION: encephalomyocarditis virus
                                                                                                                                                                                                                               TITLE OF INVENTION: Hepatitis C virus Cell Culture & TITLE OF INVENTION: Hepatitis C virus Cell Culture & FILE REPERBACE: all sequences GOOSTAND TO THE REPERBACE: all sequences CURRENT APPLICATION NUMBER: US 09/539,601C CURRENT FILING DATE: 2001-08-30 EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY EARLIER PILING DATE: 1999-04-03 NUMBER OF SEQ ID NOS: 51 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: 100.25 LENGTH: 11076
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OTHER INFORMATION: construct 1389/Core-3'/5
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2319 TGCCCGGTTGCTCCTTTTCTATCTTCCTTTTGCCTTTTGCTGTTTTGACCATCCCAG 2377
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APPLICATION NUMBER: US/08/470,426B FILING DATE: 06-JUN-1995 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-153402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAAGGTTTTGATTGTGATGCTACTCTTTGC 632
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                     CTGCTCTCTGCTCCGCTATGTACGTGGGAGATCTCTGCGGATCTGTTTTCCTCGTCGCCC 2677
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                                                                                                               422 ATCCCGCCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA
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LOCATION: (1813)..(10845)
OTHER INFORMATION: hepatitis C virus polyprotein from core to OTHER INFORMATION: nonstructural protein NS5B; carries cell culture OTHER INFORMATION: adaptive mutations from clone no. 19
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APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System;
FILE REFERENCE: all sequences
CURRENT PILING DATE: 2001-08-30
EARLIER PILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 11076
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NAMEN/KEY: RBS
NAMEN/KEY: RBS
OCCATION: (1202)...(1812)
OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
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OTHER INFORMATION: hepatitis C virus core - neomycin
OTHER INFORMATION: phosphotransferase fusion protein
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OTHER INFORMATION: construct I389/Core-3'/19
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Patent No. 6630343
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US-09-539-601-31
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NAME/KEY: 3'UTR
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PRIMERS, AND THEIR HIGH-FIDELITY DETECTION OF NON-A, NON-B 2437 2497 2557 2558 GGAACGCTAGCGTCCCCACTACGACGATACGACGCCATGTCGATTTGCTCGTTGGGGGGG 2617 2618 CTGCTCTCTCTCCTCCGCTATGTACGTGGGGAGATCTCTGCGGGATCTGTTTCCTCGTCGCCC 2677 2678 AGCTGTTCACCTTCTCGCCGCCGCCACGACACAGTACAGGACTGCAATTGCTCAATAT 2737 2738 ATCCCGGCCACGTGACAGGTCACCGTATGGCTTGGGATATGATGATGATGATGATGTCACCTA 2797 2857 2917 241 301 361 421 481 601 2498 GCGTTCGGGGAGAACAACTCCTCCCGCTGCTGGGTGGGTCACTCCCCACGCTCGCGGGCCA 182 GCGTTCGGGAGAACAACTCTTCCCGCTGCTTGGGTAGCGCTCACCCCCACGCTCGCAGCTA GGAACGCCAGCCTCCCCACCACCACAATACGACGCCACGTCGATTTTGCTCGTTGGGGCGG 2798 CAGCAGCCCTAGTGGTATCGCAGTTACTCCGGATCCCCACAAGCTGTCGTGGATATGGTGG 2858 CGGGGCCCATTGGGGAGTCCTAGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGG 482 CAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGG 542 CGGGGCCCATTGGGGAGTCCTGGCGGCCTCGCCTACTATTCCATGGTGGGGAACTGG CTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTCTTCCTCGTCTCCCC 422 ATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTA 362 AGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCT

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OLIGONUCLECTIDE PRIMERS, AND THEIR APPLICATION OF NON-A, HEPATITIS VIRUS
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TITLE OF INVENTION: OLIGONUCLECTIOR PRIMERS, AND THEIR TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF INVENTION: HEPATITIS VIRUS NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSE: Beveridge, DeGrandi, Weilacher & Young, ADDRESSEE: L.L.P. STREET: 1850 M Street, N.W., Suite 800 CIIT: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
CLASSIFICATION OF 336
PRIOR APPLICATION NUMBER: UP 2-153402
PILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 20,531
TRIECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.8%; Score 563.8; DB 2; 93.3%; Pred. No. 3.2e-140; ive 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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nucleic acid
IDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 589; Conservative
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Pred. No. 3e-140;
0; Mismatches 42;
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                                                      NAME: Wellacher, Robert G.
REGISTRATION NUMBER: 20,531
REPERRENGE/DOCKET NUMBER: 06/59-47083.1
TELECHONE: (202) 659-2811
TELEPRAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1539 base pairs
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3.08-470-426B-14
5.Sequence 14, Application US/08470426B
5.Patent No. 5856458
6.GENERAL INFORMATION:
7.APPLICANT: Okamoto, Hiroaki
7.APPLICANT: Nakamura, Teteuo
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.3%;
Matches 589; Conservative
     FILING DATE: 12-JUN-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid_
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
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                                                       GCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTA
                                                                                     CGGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGAACTGGG
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                                                                                                                                                                                               RESULT 15
US-08-081-072-18
is Sequence 18, Application US/08081072
is Patent No. 5641654
is GENERAL INFORMATION:
APPLICANT: NO. 5641654 and Michinori KOHRA.
APPLICANT: TOYOSHIMA, and Michinori KOHRA.
ITILE OF INVENTION: NON-B HERALITIS-SPECIFIC
ITILE OF INVENTION: NON-B HERALITIS-SPECIFIC
ITILE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman
STREET: 1310 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 559; DB 1; Length 742;
Pred. No. 4.7e-139;
0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: USA

ZIP: 02109-4280

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk,3.50inch,1.4MD storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh Classic
SOFTWARE: Microsoft Word Version 4.0A
CURRENT APPLICATION NUMBER: US/08/081,072
FILING DATE: June 22, 1993
INFORMATION FOR SEQ ID NO. 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 742 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: TANDEDNESS: double
                                                                                                                                                    CTAAGGTTTTGATTGTGATGCTACTCTTTGC 632
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92.9%;
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Matches 586; Conservative
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                                                                                     CTGCTCTCTCTTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCC
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Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions
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                                                                                                                                                                                                                                                                                                                                                                                                                  pending databases have been split into two parts to reduce the amount of time required for their daily
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/cgn2_6/ptodata/2/pna/US6053_COMB.seq:<sup>,</sup>
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GenCore version 5.1.6
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June 16, 2004, 08:32:08 ; Search time 2425.41 Seconds (without alignments) 14206.949 Million cell updates/sec Run on:

US-09-899-303A-5 795 1 ATGITGGGTAAGGTCAICGA.....TACTCTTTGCTCCCTAATAG 795 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

6940544 Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database

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90 ba: *
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

PAT 07-MAR-1997

linear

DNA

795 bp Sequence 5 from Patent #09604385. A48667 A48667.1 GI:2302380 RESULT 1
A4867
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS

unidentified
unclassified.
1 (base 1 to 795)
Maertens,G., Bosman,F., De,M.G. and Buyse,M.
PURIPIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
Patent: WO 9604385-A 5 15-FEB-1996;

JOURNAL

TITLE

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PAT 17-0CT-2001
CTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCG 720
                                                                                                                                                                                                                                                                                         Unclassified.

1 (bases 1 to 795)

Meartens,G., Bosman,F., De Martynoff,G. and Buyse,M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use
                           ATGITIGGGTAAGGICATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
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                                                                    /organism="unidentified"
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1. 792
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             Other publication CA 2172273 960215
Other publication AU 3382495 960304
Location/Qualifiers
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Maertens,G., Bosman,P. and Buyse,M.A.
Purified Hepatitis C Virus envelope proteins for diagnostic therapeutic use
Patent: WO 0.205558-A 5 18-JUL-2002;
INNOGENETICS N V. (BE)
Location/Qualifiers
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/organism="Hepatitis C virus"
/organism="Hepatitis C virus"
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/note="unnamed protein product"
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Viruses; ssRNA positive-strand viruses,
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Sequence 5 from Patent WO02055548.
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QLLRIPQAVVDWVAGAHWGVLAGIAYYSWVGNWAKVLIVMLLPAP"
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Hepatitis C virus
Viruses; s8RNA positive-strand viruses, no DNA stage; Flaviviridae;
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GDLCGSVFINSQLFTTSPREHBTYODCNCSIYPGHTTGRRAMDMMWRSPTTALVVS
OLLRIPQRAVDMVAGAHWGVLAGLAYSMVGNWARVLIVMLIPAP"
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/codon_start=1
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Viruses; ssRNA positive-strand viruses,
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IMHTPGCVPCVPERNNSSRCWVALTPTLAARNASVPTTTIRRHVDLLVGAAAFCSAMYV
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GLLRIPQAVVDKVAGAHWGVLAGLAYYSMVGNWAKVLIVMLLFAP"

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Maetrens,G., Boman,F., De Martynoff,G. and Buyse,M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use
Patent: US 6245503-A 47 12-JUN-2001;
Location/Qualifiers
1. 2082
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Sequence 47 from patent US 6245503.
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db_xref="CI:2302423"

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SDTRGIVSLFSPRGSAQXIQLNYTNGSNHINRTPALNCNDSLQYCGFRAALFYRHVSGAAA

SDTRGIVSLESPRGSAQXIQLNYTNGSNHINRTPALNCNDSLQYCGFRAALFYRHVRNSSG

CPERLASCRSIDKFAQGWGPLTYTEPNSSDQRPYCWHYARPRCGIVPASQVCGPVYCF
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PCH IGGAGNNTI. TCPTDCFREHPBATYAR CGSGPWI.TPR CWHYPYRI.WHYPCTVNPT
FRVWNYGGVEHR FRAACNWTRGERCEDLEDRDRESELS PLILESTTEWDI. ILLOSTREWOLD LECSFTTLP
ALSTGLI. HILJQNI VOYOY LYCGSAVVSLVI KWRYVI.LI. FTLI.ADARI CACLIMMALLI.
AQABAALENI. VVLNAAAVAGAHGTI.SPI.VFFCAAWY I KGRI. VPGAAYAFYGWPLILLI.
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Maertens, G., Bosman, F., De, M.G. and Buyse, M.
Maertens, G., Bosman, F., De, M.G. and Buyse, M.
Maertens, G., Bosman, F., De, M.G. and Buyse, M.
THERAPEUTIC USE
Patent: WO 9604385-A 47 15-FEB-1996;
INNOGENETICS NV (BE)
Other publication CA 217273 960215
Other publication AU 3382495 960304.
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                                                                         ATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTG
                                                                                                                                           CTCCGGATCCCACAAGCTGTGGACTGGTGGCGGGGGGCCCATTGGGAGTCCTGGCG
ATGCCTTGGGATATGATGATGATGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTG
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Pred. No. 1.2e-163;
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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                                   and Buyse, M.A.
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                                                                                                                                                              /note="unnamed protein product"
/codon_start=1
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Mertens, G., Bosman, P., de Martynoff, G.
Recombinant vectors for producing hov er
Patent: EP 1211315-A 47 05-JUN-2002;
Innogenetics N.V. (RE)
 Viruses; ssRNA positive-strand viruses,
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/db_xref="taxon:11103"
                                                                                   Location/Qualifiers

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              Hepacivirus.
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Pred. No. 1.2e-163;
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/mol_type="unassigned DNA"
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/protein id="CAD86535.1"
/brotein id="CAD86535.1"
/db xref="GI:GAD86535.1"
/db xref="GI:GAD86535."
/db xref="INGKVIDTLTCGPADLWGYIPLWGAPLGGAARALAHGWRVLEDG
/translation="NLGKVIDTLTCGPADLWGYIPLWGAPLGGAARALAHGWRVLEDG
WNYATGNLPGCSFSIFILALSCLTPRASAYFORNVSGWYHYTNDCSNSSIVYEAADM
WNYATGNLPGCSFSIFILALSCLTPGTTTTRHYDLLUGAAAFGSAMYW
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Purified Hepatitis C Virus envelope proteins for diagnostic and
GACCTCTGCGGATCTGTCTTCCTCCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
                                                        CGGATCCCACAAGCTGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGGT
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/note="unnamed protein product"</pre>
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Hepatitis C virus
Viruses; BSRNA positive-strand viruses,
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/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_tref="taxon:11103"
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Patent: WO 02055548-A 47 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Sequence 47 from Patent WO02055548.
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CTCGTCGGCGCCCCCCTAGGGGGGCGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG
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Patent: WO 03051912-A 47 26-JUN-2003;
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0; Mismatches 2;
                                                                               note="unnamed protein product"
                        /organism="Hepatitis C virus"
mol type="unassigned DNA"
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Macreens G., Bosman, P., De, M.G. and Buyse, M.
Macreens G., Bosman, P., De, M.G. and Buyse, M.
PURIFIED HERATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
PATENT: WO 9604385-A 49 15-FEB-1996;
INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304.
                                                                                                                                                              CEGATICCCACAAGCTGTGGTGGACATGGTGGCGGGCCCCATTGGGGAGTCCTGGCGGGT
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               TIGGCTTTGCTGTCCTGTCTGACCGTTCCGCTTATGAAGTGCGCAACGTGTCC
                                                            TTGGCTTTGCTGTCCTGTCTGAACCGTTCCGCTTCCGCTTATGAAGGGCGCAACGTGTCC
                                                                                               GGGATGTACCATGTCACGAACGACTGCTCCAAGCATTGTGTATGTGTATGAGGCAGCGGAC
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Maertens,G., Bosman,F., De Martynoff,G. and Buyse,M.-A.
Purified hepatitis C virus envelope proteins for diagnostic
therapeutic use
Patent: US 6245503-A 49 12-JUN-2001;
Location/Qualifiers
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/mol_type="unassigned
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AR157351.1 GI:16218285
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Query Match

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Pred. No. 1.2e-163;
0; Mismatches 2;
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Viruses; ssRNA positive-strand viruses,
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GVRATRKTSBR&QPRGRRQD:DFXARPEGRAMAPQCYPWPLYGREGWAMAGMLLSPRG
GVRATRKTSBR&QPRANLGKVIDTLTCGFADLVGYIPLVGAPLGGAARALAHGYVLED
GVNYATGNLPGCSFSIPLLALLSCLTVPASAYEVRNVSGMYHVTNDCSNSSIVYBAAD
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VGDLCGSVPLVSQLFTISPRRHBTVQDCNCSIYPGHITGHRMAMDMMMWSPTTALVV
SQLLRIPQAVVDMVAGAHWGVLAGLAYYSWVGNWAKVLVVWLLPAGVDGHTRVSGGAA
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GCPERLASCTSIDKFAQGWGPLITYTENSSDQBTYCMHTARRPROGITWANGTGPTKUCGG
PTESPVYCTTDRFGVPTTNWGANDSDVLILNNTRPPRGNWFGCTWMNGTGFTCUGG
PCNIGGAGNNTLIPCPTDCFRKBLBATYARCGSGPWLIPRCMTHYPYTLMHYPCTVNF
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PALSTGLIHLHONIVDVQYLYGVGSAVVSLVIKWEYVLLLRLLADARICACLMMMLL
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Recombinant vectors for producing how envelope proteins Patent: EP 1211315-A 49 05-JUN-2002; Innogenetics N.V. (BE)
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Pred. No. 1.2e-163;
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                                                                                                                                                'note="unnamed protein product"
                                                                                                                                                                             /protein id="CAD38083.1"
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/db_xref="REMTREMBL:CAD38083"
                                                                              /organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/mol_type="taxon:11103"
/d_z430
                                                 Location/Qualifiers

    1. .2427
    /product="unnamed"

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PAT 29-MAR-2003
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Plaviviridae;
Hepacivirus.
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IAQARAALENIVVLANAAVAGAHGTLSFLVFFCAAWYIKGRLVPGAAYAFYGVWPLLL
LLLALPPRAYA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maertens, G., Bosman, F. and Buyse, M.A.
Purified Hepatitis C Virus envelope proteins for diagnostic and
                  895 GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
                                                                                                      955 GCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
544 GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACGTATG
                                                                               GCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
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Pred. No. 1.2e-163;
0; Mismatches 2;
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/codon_start=1
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Patent: WO 0205548-A 49 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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49 from Patent WO02055548.
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/organism="Hepatitis C vir.
/mol type="unassigned DNA"
/db_xref="taxon:11103"
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/product="unnamed"
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FEATURES Location/Qualifiers Source 12433 "Hepatitis C virus" //organism="Hepatitis C virus"/mol type="mnassimpasimpasimpasimpasimpasimpasimpasim	a	/codon gtart=1 /protein id="CAB88259.1" /db.xref="G13.37515782" /tb.xref=dian=18715782"	/ LIBSACLION BINSACLION WARKE GOVERNOON TO TOO TO TOO TO TOO TO TOO TO TOO TO	MURITIESCUP VERNISSRCWAVALIP I LIARKINGAN PULLUKARFICSSANI VGDLGGSVPLVSQLPTI SPRRHETVOCONSI I PGFI I I IKRUPADANGNSPTTALIVV SQLLR I PQAVVDMVAGAHWGVLAGLAYY SMVGNWARVLVVMLLFAGVDGHTRVSGGAA ASDTRGLVSLESPEGSAQNI QLVMTNGSHT INRTALIVODSLGTSPPRALIFSKENS CODER I ROGET INVENGORGH TAVERDING GNORD CALVA DE BOCT UND SCHUCHVO	GUERMINGGERINTENGRANDELLI I I ERRUSINGKET CHAF HAR FOLGIV FRAGOUGET CO FTPSEYVVOGTTDTREGVETVINGANDSDVI. ILNITREPERGIMPEGCTMINGTGETKTCGG PPCNI GGAGNNTI. TCPTDCPRKHPRATYARCGSGPWL/TPRCMVHY PYRLWHY PCTVNP TI PKYRMYTVGEROLDERDRICHER BERACHWINGERED GERESPELLETTENGUETTENGUET DAN 18 THE DELIB THE DAN 18	IAQABBALIENIAVILNAAVAGAHGTLSFLVFFCAAWYIKGRLVPGAAXAFYGVWPLLL LILALPPRAXA" 12427 //xxxdint = hvmnamed"	/ Match 98.0%; Score	Best Local Similarity 99.7%; Pred. No. 1.2e-163; Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps	Oy 4 TYGGSTAAGGTCATCATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGGTACATTCCG 63 Db 355 TYGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCGGACCTCGTGGGGTACATTCCG 414	by 64 createseaccccccraegeseacraecaseacccraegeseargecargatic 123	415	GAGGACGCGCGAACAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC		Db 535 TIGGCTTIGCTGTCTGACGGTTCCAGGCTTCCGCTTATGAAGTGCGCAACGTGTCC 594 Qy 244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC 303	Db 595 GGGATGTACCATGTCACGAACGACTGCTCCAACGCATTGTGTATGAGGCACGGGAC 654	Qy 304 ATGATCATGCACACCCGGGGTGCCTGCGTTCGGGAACAACTCTTCCCGCTGC 363 1	364 TGGGTAGCGCTCACCCCCACGCTCGCAGCAACGCCAGCGTCCCCACCACCACTATA	Oy 424 CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG 483	484 GACCTCTGCGATCTGTCTCCTCGTCTCCCCAGCTGTTCACCATCTCGCCTCGTCTCTCTC	835 GACCICIGOSGAICTICITICCTOGAICTICICCAGCTGTTCACCATCTCGCCTCGCCGGGGAT	Oy 544 GACACGTYCCAGAATTGCTCAATTCCCGCCACATAACGGCTACCGTATT 603 Db	
Db 355 TIGGGTAAGGTCAICGAIACCTIACAICGGGTTCGCCGACTCGTGGGGIACAITCCG 414 OV 64 CICGGGGGCCCCCCTAAGAGAGAGAGAGAGAGAGAGAGAGAG	415 CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGATGCGGTTCTG	OY 124 GAGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTCTCTTTCTCTC 183	OY 184 TYGGCTTYGCTGTCTCTCTCTGTCTCCGCTTATGAAGTGCGCAACGTGTCC 243	Qy 244 GGGATGTACCATGTCA.CCAACCGACTGCTCCAACTCATGTATGAGGCAGCGGAC 303 Db 595 GGGATGTACCATGTCA.CGAACGACTGCTCCAACTCAAGCATTGTGTATAGAGGAGCGAC 654	Dy 304 ATGATCATGCACCCCGGGTGCGTTCGGGTTCGGGAACAACTCTTCCCGCTGC 363 Db 655 ATGATCATGCACACCCCGGGTGCGTGCGTTCGGGAACAACTCTTCCCGCTGC 714	Qy 364 TGGGTAGCGCTCACCCCCACGCTCGCAGCTCCCCACCACCACACAATA 423 Db 715 TGGGTAGCGCTCACCCCCACGCTCGCAGCTCCCCACCACCACAATA 774	Qy 424 CGACGCCACGTCGATTTGCTCGTTTGGGGGGGGCTGCTTTTCTGTTCCGCTATGTACGTGGGG 483 Db 775 CGACGCCACGTCTGGGGGCGGGCTGCTTTTCTGTTCCGCTATGTACGTGGGG 834	484 GACCTCTGGGGATCTGTCTTCGTCTCCCAGCTGTTCACCATCTCGCCTGGCAT	Db 835 GACCTCTGCGGATCTTCCTCGTCTCCCAGCTGTCCACCATCTCGCCTGGCGGGAT 894 Oy 544 GAGACGGTGCAGAGTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG 603	Db 895 GAGACGGTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG 954	Qy 604 GCTTGGGATATGATGATGATCGCTACAACGCCCTACAACGCCCTGGTGGTATCGCAGCTGCTC 663 Ab	664 GGGATCCCACAAGCTGTGACATGGTGGGGGGGGCCCATTGGGGAGTCCTGGCGGGT	Db 1015 cedarcccacaaecreresedacaresedesedesedesederesedasedesedesedesedesedesedesedesedesed	QY 724 CTCGCCTACTATTCCATGGGGAACTGGGCTAAGGTTTTGATTGTGATGCTACTCTT 783 Db 1075 CTCGCCTACTATTCCATGGGGAAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTT 1134	Qy 784 GC 785	Db 1135 GC 1136	AX794892 LOCUS AX794892 LOCUS AX794892 DEFINITION Sequence 49 from Patent WO03051912.	SO SO	SOURCE REPAILITE C VITUS ORGANISM Hepatitis C virus Organism Serna positive-strand viruses, no DNA stage; Flaviviridae;	REFERENCE 1 TOPOLO 1 NOTHORS Maertens, G., Depla, E. and Bosman, F.		INNOGENETICS N.V. (BR)

ò	604 G	604 GCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC 663
QQ	955 G	
ò	664 0	664 CGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGGGT 723
đ	1015 C	1015 GGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCATTGGGGAGACCCTGGCGGGC
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qq	1135	1135 GC 1136
Search Job ti	Search completed: June Job time : 2427.41 secs	Search completed: June 16, 2004, 11:39:16 Job time : 2427.41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

June 16, 2004, 07:39:53 ; Search time 299.119 Seconds (without alignments) 11290.892 Million cell updates/sec Run on:

US-09-899-303A-5 795 1 ATGTTGGGTAAGGTCATCGA.....TACTCTTTGCTCCCTAATAG

score: Title: Perfect

Sequence:

795

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* Database

genesegn1980s:* genesegn1990s:* genesegn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length	DB	ID	Description
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0	767.8	9.96	2434	9	AAL48940	Aal48940 Hepatitis
10	703.6	88.5	9605	9	ABK91431	Abk91431 Hepatitis
11	703.6	88.5	9605	9	ABK91424	Abk91424 Hepatitis
12	703.6	88.5	9605	9	ABK91429	Abk91429 Hepatitis
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15	703.6	88.5	9605	9	ABK91430	Abk91430 Hepatitis
16	703.6	88.5	9605	9	ABK91428	Abk91428 Hepatitis
17	703.6	88.5	9605	9	ABK91425	
18	703.6	88.5	9605	9	ABK91426	Abk91426 Hepatitie
19	703.6	88.5	9605	9	ABK91433	Abk91433 Hepatitis
20	703.6	88.5	9605	9	AAD25332	Aad25332 Hepatitis
21	703.6	88.5	9608	9	ABK91427	Abk91427 Hepatitis
22	703.6	88.5	11062	9	AAD25331	Aad25331 Hepatitis
23	703.6	88.5	11076	m	AAA98965	Aaa98965 Hepatitis

Aba03491 Cuticle p Aaq43889 NANB hepa Aaq63753 NANBHV ge Aaq24467 NANB hepa		Aaq29628 Frasmin p Aaq29628 Hepatitis Aav60673 Fragment		Aat03960 Partial H Aad25517 Hepatitis Aa153723 Hepatitis Aa449655 Henatitis	
ABA03491 AAQ43889 AAQ63753 AAQ2467	AAQ4068 AAT30386 AAV60672	AAQ29628 AAV60673	AAQ26981 AAQ80498 AAQ81559	AAT03960 AAD25517 AAL53723 AAD49655	AAQ15363 AAQ12242 AAQ20923 AAD33038
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22 25 26 27	0000	3 3 3 4	35 37	3 8 8 3 8 8 4 0 1	4 4 4 2 6 4 3 3 6 4 5

ALIGNMENTS

BP. AAT12705 standard; DNA; 795 (first entry) HCV El construct HCCI10A. 23-SEP-1996 AAT12705;

HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;

Hepatitis C virus.

WO9604385-A2

15-FEB-1996.

95WO-EP003031. 31-JUL-1995; 94EP-00870132. 29-JUL-1994;

(INNO-) INNOGENETICS NV.

Buyse M; De Martynoff G, Bosman F, Maertens G,

WPI; 1996-129401/13.

Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.

Claim 23; Fig 21; 146pp; English.

and B2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant B1, B2, and B1/B2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or in reduction step with a disulphide constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more

BP

795

AAL48914 standard; DNA;

AAL48914;

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serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed BI, R2 and BI/R2, and sliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
                                                                                                                                                                                                                               ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody the tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                           The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV B1 or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chromic HCV infected mammal. The present DNA sequence encodes an HCV B1 protein.
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100.0%; Score 795; DB 9; I
Best Local Similarity 100.0%; Pred. No. 4.1e-204;
Matches 795; Conservative 0; Mismatches 0;
    Example 1; SEQ ID NO 5; 271pp; English
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liver fibrosis; ds; gene.
TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
                                                                              TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACA
                                                                                           ATACGACGCCACGTCGATTTGCTCGTTGGGGCGCCTGCTTTCTGTTCCGCTATGTACGTG
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liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal
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P-PSDB; ADD55514.
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                                                        ATGATCATGCACACCCCCGGGTGCGTGCCTGCGGTTCGGGGAACAACTCTTCCCGCTGC 363
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 244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC 303
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liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal
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16-OCT-2002; 2002US-0418358P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or E2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in viro monitoring of HCV disease or prognosing the response to in viro monitoring from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans from
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                                                                                                           Hepatitis C virus E2 protein related coding sequence SEQ ID NO: 47
                                                                                                                                                Hepatitis C virus; HCV; B1 protein; E2 protein; infection; gene;
virucide; immunostimulant; vaccine; ds.
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llarity 99.7%; Pred. No. 1.3e-199;
Conservative 0; Mismatches 2;
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AAL48939 standard; DNA; 2082 BP
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30-AUG-2001; 2001US-0315768P.
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P-PSDB; AAO18678.
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wes 780; Conserv
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                                                                                                                                                                                              124 GAGGACGCCTGAACTATGCAACAGGGAATTTGCCCCGGTTGCTCTTTCTCTTTTCTCTT 183
                                                                                                                                                                                                                                     GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC 303
                                                                                                                                                                                                                                                                                                                     ATGATCATGCACACCCCCCGGGTGCGTGCCTTCCGGAGACAACTCTTCCCCGCTGC 363
                                                                                                                                                                                                                                                                                                                                                                                          TGGGTAGCGCTCACCCCCACGCTCGCAGGTAGGAACGCCAGCGTCCCCACCACGACAATA 423
                                                                                                                                                                                                                                                                                                                                                                                                    364 TGGGTAGCGTCACCCCACGCTCGCAGCTAGGAACGCCAGCTCCCCACGACAATA 423
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                                                                                                                                                              4 TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG 63
                    The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV B1 or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present DNA sequence encodes an HCV E1/E2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACGCCACGTCGTTTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG
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                                                                                                 98.0%; Score 778.8; DB 9; Length 2082;
                                                                              Sequence 2082 BP; 366 A; 634 C; 600 G; 482 T; 0 U; 0 Other;
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                                                                                                           Pred. No. 1.3e-199
0; Mismatches 2
 SEQ ID NO 47; 271pp; English.
                                                                                                          Best Local Similarity 99.7%;
Matches 780; Conservative
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and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more serotyping assay for detecting one or more can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates containing proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope proteins - in presence of d1:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.
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                                                                                                                                                                                                                                            HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human;
serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maertens G, Bosman F, De Martynoff G,
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AAT12973 standard; DNA; 2086
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and R2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. In vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide constructs containing the purified RCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed B1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more centive with human sera than those isolated by known techniques
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- in presence of dissulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 U; 0 Other;
                                                            Claim 23; Fig 21; 146pp; English.
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Local Similarity 99.7%;
hes 780; Conservative (
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                        CTCGCCTACTATTCCATGGGGGAACTGGGCTAAGGTTTTGATTGTGATGCTACTTTT 783
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475 GAGGACGCGTGAACTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises an Hepatitis C virus (HCV) vaccine for reducing liver disease. The vaccine of the invention comprises an HCV El or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present DNA sequence encodes an HCV El/E2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; vaccine; liver disease; El protein; E2 protein; liver fibrosis; ds; gene.
CGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAAGTCCTGGCGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2433 BP; 434 A; 745 C; 714 G; 540 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus B1/B2 protein coding sequence #14.
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16-OCT-2002; 2002US-0418358P.
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P-PSDB; ADD55558.
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The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRBS) region coding for one or more NS3, NS5A, or EMCV IRBS mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV
                                                                                                           New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRBS) region, useful in studying HCV replication and
                      1015 CCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
CCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGCCCCATTGGGGAGTCCTGGCGGG
                                                                                       723 TCTCGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTTGATTGTGATGCTACTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "The polyprotein" NS2, NS3, NS4B, NS5A and NS5B proteins" replace(6934,T) /*tag= b
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                                                                                                                                                                                                                                                                                          RESULT 10
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                                                                                                                                                                                                                The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific Oilgomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention
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                                                                  New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2434 BP; 434 A; 745 C; 714 G; 541 T; 0 U; 0 Other;
                                                                                                                                                                              Example 2; Page 212-215; 243pp; English
    WPI; 2002-599657/64..
P-PSDB; AAO18679.
                                                                                                                                     HCV infection.
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replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV replicon Con 1 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV sequence appearing as ABK91411 and the information in Claim 9
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0; Mismatches 49; Indels
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The invention relates to mucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (BMCV) internal ribosome entry site (IRRS) respon coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a mucleotide sequence coding for the altered nucleic cacids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids (2) a recombinant cell produced by introducing an HCV (hepatitis C virus) cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) caplicon enhanced cells made in the method; and (6) measuring the ablity of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and HCV replicon enhanced cells are useful in studying HCV replication and HCV and host cell interactions, producing HCV RNA and concludate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and compound to more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and compand of the invention. Note: The present sequence is an HCV replicon Con 1 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRBS) region, useful in studying HCV replication and
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                                                                                                                                                                      HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
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                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "HCV polyprotein"
/note= "The polyprotein consists of the Core,
NS2, NS3, NS48, NS48, NS5A and NS5B proteins"
/*tag= b
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                      ABK91424 standard; DNA; 9605
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Synthetic.
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                                                          ABK91424;
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Key
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88.5%; Score 703.6; DB 6; Length 9605;

Query Match

GC 1477

B2, P7,

B1,

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The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS54, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and proteins, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to more HCV activities e.g. to discover drugs which may the HCV mediated diseases ment as laver failure, cirthosis and
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                                                                                                                   /notes "The polyprotein"
NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
/tag= b
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/*tag= a
/product= "
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                     Hepatitis C virus.
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                     733; Conservative
Best Local Similarity
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The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (TRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression certor comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV acivity. The HCV replicans and HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV acivity. The HCV replication and expression, and HCV and host cell interactions producing HCV RNA and expression, and HCV and host cell interactions producing HCV RNA and combinate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and compound to motellular carcinoma. The present sequence is an HCV replication in the appearing as ABK91411 and the information in Claim 9
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New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRBS) region, useful in studying HCV replication and

Claim 9; Page; 69pp; English.

expression.

(RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.

16-JAN-2002; 2002WO-EP000526 23-JAN-2001; 2001US-0263479P

WO200259321-A2

Paonessa G;

De Francesco R, Migliaccio G,

WPI; 2002-599793/64.

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Seguence 9605 BP; 1911 A; 2883 C; 2732 G; 2079 T; 0 U; 0 Other;
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                                DB 6; Length 9605;
                               / Match 88.5%; Score 703.6; DB 6; Length Local Similarity 93.7%; Pred. No. 4e-179; hes 733; Conservative 0; Mismatches 49; Indels
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HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRBS; NS5A; HCV replication; mutant.

Hepatitis C virus Con 1 isolate DNA mutant 9.

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B2,

E1,

/product= "HCV polyprotein" /note= "The polyprotein consists of the Core, NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins" replace(6936,G) /*tag= b

mutation

Location/Qualifiers 342. .9374

Hepatitis C virus.

Synthetic

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The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (TRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic caids which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell broadcade by introducing into a human hepatoma cell the altered mucleic acids (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method, and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV and host cell interactions, producing HCV RAB and expression, and HCV and host cell interactions, producing HCV RAB and ceptression, and providing a system for measuring the ability of a compound to more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and chaptacedlular carcinoma. The present sequence is the HCV replicon Con 1, used as a basis for the adaptive mutations of the invention
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NSS encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and
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                                                                         Claim 9; Page 36-39; 69pp; English.
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Matches 733; Conservative
                                      expression.
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                                                                                                              1116 CGACGCCAFGTCGATTTGCTCGTTGGGGGGCTGCTCTCTGCTCCGCTATGTACGTGGGA
                                                                                                                                                                                                                                                                                                                                         1296 GCTTGGGATATGATGAACTGGTCACCACAGGCGCTAGGGGTATCGCAGTTACTC
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                                            .056 TGGGTAGCGCTCACTCCCACGCTCGCGCCAGGAACGCTAGCGTCCCCACTACGACGATA
                                                                                           CGACGCCACGTCGATTTGCTCCTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG
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                   TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACCACAATA
                                                                                                                                                                    GACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCV; ds; Con 1; adaptive mutation; liver failure; cirrhosis; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NS5A; HCV replication.
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/note= "The polyprotein consists of the Core,
NS2, NS3, NS4A, NS4B, NS5A and NS5B proteins"
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          The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids (3) a recombinant cell produced by introducing into a human hepatoma
                                                                             783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and
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GCTTGGGATATGATGATGACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
                                       CGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGGGT
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NS2, NS4A, NS4B, NS5A and NS5B proteins"
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Synthetic.
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cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and mutant of the invention. Note: The present sequence is an HCV replicon Con I mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV sequence appearing as ABK91411 and the information in Claim 9
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AV392165 AV392465
B1996341 1031037A0
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C72860 C72860 Rice
CC010084 PUGJJ92TB
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Tex: 86-21-50801922
Exa: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV755731 AW Homo sapiens cDNA clone BMFAKB03 5', mRNA sequence
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CB640103
CB668031
BM017656
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BNG69967
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CC605518
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CA659369
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CD432549
BJ536071
CNS010C9
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AV755731 AV755731
AV758366 AV758366
BX356664 BX356664
AL053013 Drosophil
                                                                                                                                      June 16, 2004, 09:12:53 ; Search time 2137.22 Seconds (without alignments) 11108.065 Million cell updates/sec
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1 ATGITGGGTAAGGTCATCGA......TACTCTTTGCTCCTAATAG 795
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Compugen Ltd.
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                 GenCore version
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1 (bases 1 to 492)
Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Rao,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Pu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Ran,Z. and Homo sapiens cDNA BM clones
Unpublished (2000)
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Contact: Zeguang Han
Contact: Zeguang Han
State Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919
Fax: 86-21-50801922
Email: hanzgedng-sh.cn
This clone is available at CHGC in Shanghai.
                                                                        /clone="BMFAKB03"
/tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab host="BME5.8"
/clone_lib="BM"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
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AV758366
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/mol_type="mRNA"
                              /organism="Homo sapiens"
/mol_type="mRNA"
                                                               /db_xref="taxon:9606"
 Socation/Qualifiers
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1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="cs001015xB03"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="trand cDNA was primed with a Not1-oligo(dT)
/primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
/tissue_type="Bone marrow"
/cell type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BMS.8"
/clone_lib="BMN"
/note="Vector: pTriplEx2; Site_l: sfillA; Site_2: sfil8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 TCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                              461 TCTGTTCCGCTATGTACGTGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCCAGCTGT
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BP 191 91006 BVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com Uhttp://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIOISCAOLNPI.
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                                                                                                                                                                                                                                                                     Length 492;
                                                                                                                                                                                                                                                                 11.5%; Score 91.6; DB 9; Length 49
60.9%; Pred. No. 4.1e-10;
vative 0; Mismatches 114; Indels
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 ENTY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster and project of the Drosophila melanogaster and please see http://www.fruitfly.org The BDGP Drosophila melanogaster at the Library was prepared by Kazucyo Osoegawa and melanogaster at the Rowell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                        SSBTBSYTBSSSTSSSSSSBBTTTSSSTSSSTSSSSTTSBSSSTTTSBSS
                                                                                                                                                                                                                                                          SSTSBSBTTSCTTTTKSBSSSTBSTSSTTSTBTSCTTTBSSTTBYTBSSSYBSBSSBTTS
                                                                                                                                              CCCTTACATGCGGCTTCGCCGACCTCGTCGGGGTACATTCCGCTCGTCGGCGCCCCCTAG
                                                                                                                                                                                                                                                                                                                      TGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCCGGGATGTACCATGTCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa, Arthropoda; Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 TCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGG
                                                              Length 1201;
                                                                                                        Indels
                                                           5.9%; Score 47.2; DB 13;
larity 10.7%; Pred. No. 6.1;
Conservative 250; Mismatches 227;
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Drosophila melanogaster
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Triticum aestivum
Enkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Wagnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Triticum.
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BCORI digestion of Drosophila DNA provided by the BDGP from the lagogenic strain y2, cn bw sp, the same strain used for the BDGP Pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allard, F., Crosby, W.L., Danyluk, J., Budes, P., Frick, M., Gaudet, E. Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Linke, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 TITITISSGGYGKGCSSGSGBSCSCCSSCSCSCSCCCCCCCCSSSBSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 CTGCTTTCTGTTCCGCTATGTACGTGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCC
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Library 5 GATE
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                                                                                                                                                                                                            melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 10.1., Mismatches Matches 70; Conservative 166; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     5.5%; Score 43.4;

    . 925
    /organism="Drosophila me/mol_type="genomic DNA"
/db_xref="taxon:7227"

                                                                                                                                                                                                                                                                                   /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TBT3"
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AL513886 Homo sapiens PLACENTA Homo sapiens CDNA clone CL0BA006ZG08 5-PRIME, mRNA sequence.
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Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length CDNA libraries and normalization Ompublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12777380.
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BP 191 91006 EVRY cedex - France
BR ali: sequeségenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4924.f For
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 FT from Amersham High quality sequence stop: 382.
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48.7%; Pred. No. 39;
iive 0; Mismatches 122;
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/db_xref="GDB:6032522"
/db_xref="taxon:9606"
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                                              Bioinformatics
University of Saskatchewan, Department of Computer Science
University of Saskatchewan, Department of Computer Science
University of Saskatchewan, S7 Campus Drive, Saskatchon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 1769
Fax: 306 966 1033
Fax: 306 966 2033
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/clone liberarulings
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/restair cardina aestivum FCAS: Library 5 GATB 7"
/note="Vector: pCMV.SPORT6; Crown and developmental stages
of spike formation in wheat cultivar Norstar. 4 mRNA
populations were combined before constructing the library.
The first mRNA population is from lom crown sections after
30 days of cold acclimation. The second is from lom crown
sections after 11 days of deacclimation (before
deacclimation plants were fully vernalized for 49 days).
The third is from different developmental stages of spike
formation [5 to 50mm] that still have not emerged from the
leaf (dissection required). The last is from different
developmental stages of spike and seed formation after
having emerged from the leaf (visible). First strand
synthesis in this library was done in the presence of
methylated dCTP thereby protecting from internal cleavage
with Not!."
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Homo sapiens
     Contact: Wm L Crosby
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AV392783
AV392783 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CM096904_r 5', mRNA sequence.
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Chlamydomonas reinhardtii
Bukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="IGF"
/note="Vector: BeloBACII, Site_l: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGOGTTCGGGAGAACAACTCCTTCCCGCTGCGTAGCGCTCACCCCCCACGCTCGCAG
                                                                                                                                                                                    Dept. of Biology, University of Pennsylvania, Philadelphia, 19104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asamizu, B., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.2; DB 28;
Pred. No. 1.4e+02;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                         Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seg primer: Sp6
Class: BAC ends
High quality sequence start: 76
High quality sequence stop: 98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Produced by Thomas Altmann*
                                                                                                                          Contact: Bcker J.
Arabidopsis Thaliana Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/strain="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                BAC End Sequences at ATGC
Unpublished (1997)
Other_GSSs: F13A13-T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="F13A13"
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AV392783.1 GI:6546999
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                                                                                                                                                                                                                                                                        Fel: 215-898-9384
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                                                                                                                                                                                                                                                                                               /db xrefe=taxon:9606"
/clone="CLOBAO06ZG09"
/rissue type="PlACENTA"
/clone lib="Homo saplens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Pive prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Contact the Not I 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1069 CCSCGKGGGGGKSSSSGSGGCCCCCGGG---GGGSSSGSSGGCCCCWAAASSSAYKKGKK 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 14-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGGGCCCTGGCGCATGGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 ATTIGCCCGGTIGCTCTTTCTCTATCTTCCTTTGGCTTTGCTGTCTGTCTGACCGTTC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1012 GKKKTTTTWMMAAATMTHTTWWTTTTTYTCTAAWGGGTAKCVAKCCCMCCCCCAMGCTS 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                952 GACSCSCCGCAADAAVCGAGMDSGAMKGSTGVGSCCTTSRCKWGGGTTSGMMVGCATTYM 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832 SGCSKGKTTKTTTKGTCGTTGAAGASMABGRTWGAGGGGGGCCCCCYCSCMCCCCCCYB 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; coreoids; eurosida eurosida el 1; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1195)
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 CCTGCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 CTAGGAACGCCAGCGTCCCCACCACCACAATACGACGCCACGTCGATTTGCTCGTTGGGG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772 BBCCCMCHCTKCSCKWCCRGACTYCCCCASSCTSYGGTCCCCCTYYSATDTTGGTYTBSB 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F13A13-Sp6 IGF Arabidopsis thaliana genomic clone F13A13, genomic
                         http://www.genoscope.cns.fr/
cgi.bin/cluster=4924.f. Contact
cgi.bin/cluster.cgi?seq=CLOBA006ZG08RP1&cluster=4924.f. Contact
Feng Liang Fmail: fliangalifetech.com VIL.;
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA006ZG08RP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGCTTCGCCGACCTCGTGGGGTACATTCCGCTCGTCGGCGCCCCCCCTAGGGGGCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.2%; Score 41.6; DB 9; Length 1201;
llarity 26.4%; Pred. No. 1.1e+02;
Conservative 114; Mismatches 206; Indels 3;
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more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
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                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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B1996341 S52 bp mRNA linear BST 25-0CT-2001 1031037A07.y2 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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(normalized), Lambda Zap II"
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Chlamydomonas reinhardtii
Bukaryota, Viridplantae; Chlorophyta, Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 552)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Punction and Regulation in
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/dev_stage="photoautotrophic growth"
/clone lib="Chlamydomonas reinhardtii C9"
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Pred. No. 1.4e+02;
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Unpublished (2001)
                                        /db_xref="taxon:3055"
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: Ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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Assanzuk. B. Nakamura, Y., Sato, S., Pukuzawa, H. and Tabata, S.
A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433
non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
                                                                                                                                                        /db_xref="taxon:3055"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
Xhol:="Vector: pBluescriptII SK-; Site_1
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/mol_type="mRNA"
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/organism="Chlamydomonas reinhardtii"
/mol.type="mRNA"
/strain="C9"
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45.3%; Pred. No. 1.2e+02;
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Xhol; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP [WH4+ - containing) and shifted to TAP - NO3- [24hrs]; H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + Sorbitol (1, 2, 6, 24 hr) and MRA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
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Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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Pred. No. 1.4e+02;
0; Mismatches 179; Indels 0
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Fax: 919 613 8177
Email: chauser@duke.edu
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DCMB Box 91000
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Durham, NC 27708-1000
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Best Local Similarity 45.3%;
Matches 148; Conservative
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Location/Qualifiers

PEATURES

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/clone lib-catonistoss // clone lib-catonistoss in (normalized), Lambda Zap II" (normalized), Lambda Zap II" // (nore-vector: pBluescript II SK-; Site I: BCORI; Site 2: // (note-vector: pBluescript II SK-; Site I: BCORI; Site 2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines CDNAs from CC-1690 cells grown to mid-log phase in TAP (HM4 - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + Sorbitol (1, 2, 6, 24 hr) PolyA mRNA was purified from each sample, pooled and cDNA synthesized 'The cDNA was directionally cloned into lambda Zap II (Stratagene) in the BCORI (5) and XhORI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with Exassist (Stratagene) phase. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
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1 (bases 1 to 525)
Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.E., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model.
Vinicallular System for Analyzing Gene Punction and Regulation in Unpublished (2000)
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'organism="Chlamydomonas reinhardtii"
                        /mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
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                                                                               /db xref="taxon:3055"
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/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/db_xref="taxon:67593"
/clone="eff8036809"
/cissue_type="mycelium"
/cell_line="p6497"
/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_lib="uSDA-IPRAS:Expression of Phytophthora sojae
/clone_lib="uSDA-IPRAS:Expression of Phytophthora sojae
genes during infection and propagation sHB"
/note="Vector: pBK-CMV; Site_1: BcoR1; Site_2: Xho1"
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Khkaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1. (bases 1 to 671)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI723733 671 bp mRNA linear EST 19-SEI 1031067F08.yl C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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                                                                      1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
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                                                                                                                                                                                                                                      RACKWARD: BK reverse primer Plate: 036 row: B column: 09 Seq primer: BK reverse primer High quality sequence stop: 534. Location/Qualifiers
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Umpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
                                                                                                                                                                                                                PORWARD: BK reverse primer
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                                                                                                                                             Email: bmtyler@vt.edu
Tyler lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript II SK-; Site 1: BCORI; Site 2: XhOI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and CDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the BCORI (5′) and XhOI (3′) sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear EST 30-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 bp mRNA linear EST 30-OCT-200: psHB036xB09f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sHB Phytophthora sojae cDNA clone sHB0358B09 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 GAACGACTGCTCCAACTCAAGCATFGTGTATGAGGCAGCGGACATGATCATGCACACCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 CGGCTGCCTGCCTTGCGGAGAACAACTCTTCCCGCTGCTGGTAGCGCTCACCCC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 GGAGGACAAGACCTGCCACCTGGAGTCATCGAGTACTGCGACCTGGGCAACCTGTCCAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACGCTCGCAGCTAGGAACGCCAGCGTCCCCACGACAATACGACGCCACGTCGATTT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                    'organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
                             DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 CTTCCTCGTCTCCCAGCTGTTCAC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACATGCGCACCCTGCTGCTCAC 306
   Contact: Elizabeth H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF846043.1 GI:38061697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tyler B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phytophthora.
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JOURNAL
COMMENT
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AUTHORS
                                                                                                                                                                                                                                                 FEATURES
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0; Gaps

EST 19-SEP-2001

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/wol type="mkNA"
/wormalized), Lambda Zap II"
/wolne lib="C. reinhardtii CC-1690, Stress II
/wormalized), Lambda Zap II"
/woll Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (kM4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H3C2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
Polyh mRNA was purified from each sample, pooled and cDNA
synthesized The cDNA was directionally cloned into lambda
Zap II (Straagene) in the Econt (5, and Xhoxi (3')
sites. pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExAssist
(Straagene) phage. The library was normalized using
method 4 describbed."
Research 6: 791-806."
                                                                                                                                                                                                                                      organism="Chlamydomonas reinhardtii"
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
                                                                                                                                                                                                  source
                                                                                                                                                      PEATURES
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0; Gaps Similarity 47.0%; Score 40; DB 12; Length 671; Similarity 47.0%; Pred. No. 2e+02; A. Conservative 0; Mismatches 140; Indels 124; Query Match Best Local Si Matches 124

ORIGIN

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GCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGAATCTGT 500 441 ઠે g

592

CITICCTCGTCTCCCAGCTGTTCAC 524 501

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Search completed: June 16, 2004, 13:27:11 Job time : 2140.22 secs

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Scoring table:

Searched:

Database

Perfect score:

Run on:

Seguence:

Sequence 21, Sequence 21, Sequence 18, Sequence 18,

us-09-899-303a-5.rni

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GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, PONS
APPLICANT: BOSMAN, PONS
APPLICANT: BUYSE, MARINOFF, GUY
TITLE OF INVENTION: PORIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PORIFIED HEPATITIS C VIRUS ENVEROPE
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STARET: 1100 NORTH GLEBE KOAD
STARET: 1100 NORTH GLEBE KOAD
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION:
CLESSIFICATION NUMBER: 32,205
REFERENCE/DOCKET WUMBER: 32,205
US-08-904-686A-11
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US-08-612-973-21
US-08-612-973-3
US-08-612-973-3
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ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/08612973; Patent No. 6150134
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HYPOTHETICAL: NC
ANTI-SENSE: NO
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LOCATION: 1
FEATURE:
NAME/KEY: 0
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Sequence 1
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-927-597-5
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US-09-539-601-11
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US-08-324-977-9
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US-08-324-977-9
US-08-315-86A-9
US-08-315-86A-9
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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ADDRESSEE: NIXON & VANDERHYB I
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
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Matches 795, Conservative
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          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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FRATURE:
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                                                                                                                                              CCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT 120
                                                                                                                                                             CCCTCGTCGCCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCCGGGTT 120
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                         100.0%; Score 795; DB 3; Length 795; 100.0%; Pred. No. 9.8e-201; ive 0; Mismatches 0; Indels
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Patent No. 6245503
GENERAL INFORMATION:
APPLICANT: MARKTENS, GERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE NARTYNOFF, GUY
APPLICANT: PUNYSE, MARXIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
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                         Query Match 100.
Best Local Similarity 100.
Matches 795; Conservative
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US-08-927-597-5
US-08-612-973-5
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PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC
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                                                                                                                   STREET: 1100 NORTH GIRBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUWTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy Aisk
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
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100.0%; Pred. No. 9.8e-201;
ive 0; Mismatches 0;
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-WAR-1996
ATTORNEY/AGENT INFORWATION:
NAME: BYRNE, THOWAS E.
REGISTRATION NUMBER: 34,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECHOMINICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELECHOMINICATION: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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0; Mismatches 2,
                                                                                                                                                                                                                 Best Local Similarity 99.7
Matches 780; Conservative
                                                                                                                                mat_peptide
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 TOPOLOGY: line
MOLECULE TYPE: C
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
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FEATURE:
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; LOCATION:
US-08-612-973-47
                                                                                  NAMB/KEY:
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                                                                                                                                                                                                                                                                                                                                CTCCGGATCCCACAAGCTGTGGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCG 720
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                                                                                                                                                CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGT
                                                                                                                                                                                                                                                                 ATGCCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTG
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                                                               ATACGACGCCACGTCGATTTGCTCGTTGGGGGGGCGCTGCTTTCTGTTCCGCTATGTACGTG
                                                                                                                              GGGGACCTCTGCGGATCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCCTCGCCGG
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APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUYSE, MARTENOFF, GU
APPLICANT: BUYSE, MARTE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TERE: FIOPPLY GLEAR
COMPUTER: INP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: DatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
PLING DATE: 11-MR-1996
CLASSIPICATION NUMBER: US/08/612,973
FILING DATE: 11-MR-1996
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOWAS B.
REGISTRATION NUMBER: 1487-10
TELEPHONE / 703) 816-4100
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
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184 TIGGCTITIGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC 243
                                                                                            244 GGGATGTACCATGTCACGAACGACGACTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC 303
                                                                                                                                                                                  ATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC 363
                                                                                                                                                                                                                  TGGGTAGCGCTCACCCCCACGCTCGCAGGTAGGAACGCCAGCGTCCCCACCACGACAATA 423
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Fatent No. 6150134
GENERAL INPORMATION:
APPLICANT: MARTHONP, GERT
APPLICANT: BUYSE, MARTHONP, GUY
APPLICANT: BUYSE, MARTHONP, GUY
APPLICANT: DE MARTHONP, GUY
TILLE OF INVENTION: PURITIED HEPATITIS C VIRUS ENVELOPE
TITLE OP INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEB: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: I BR PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIPICATION: 110FORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GC 785
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                                               Sequence 47, Application US/08927597

Fatent No. 6245503

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MARNITENS, GERT

APPLICANT: BUYEN, MARIE-ANGE

TITLE OF INVENTION: PROTFIED HEPATITIS C VIRUS ENVELOPE

TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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98.0%; Score 778.8; DB 3;
Best Local Similarity 99.7%; Pred. No. 2.5e-196;
Matches 780; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION:
PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOWAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs
LENGTH: 2082 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
...DOTHERICAL: NO
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LOCATION:
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LOCATION:
US-08-927-597-47
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724 CTCGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTTGATTGTGATGCTACTCTTT
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NOI
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NC
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAMB/KBY: CDS
                                                                                              1135 85 1136
                                                                     784 GC 785
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAMB/KEY:
COCATION:
US-08-927-597-49
                                                                                                                                           RESULT 6
US-08-927-597-49
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            REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
LOCATION: 1..2427
                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                              1..2430
                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1...2
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US-08-612-973-49
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                                                                                                                                                                                                                                                     Sequence 49, Application US/08927597
Patent No. 6245503
GENERAL INFORMATION:
APPLICANT: BOSNAN, FONS
APPLICANT: BUYSE, MARETANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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98.0%; Score 778.8; DB 3; Length 2433;
Best Local Similarity 99.7%; Pred. No. 2.7e-196;
Matches 780; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNER: VIGATION

ZIP: 22201-4714

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE: II-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, ITHOMARE: 32,205
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 32,205
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SIG-4100
INFORMATION FOR SEQ ID NO: 49:
LUMBERTERNEY: VO3) 816-4100
INFORMATION CA33 base pairs
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                                                                                                                                                                                                                      LOCATION: (1813)..(10845)
OTHER INPORMATION: hepatitis C virus polyprotein from core to
OTHER INPORMATION: nepatitis C virus polyprotein from core to
OTHER INPORMATION: nonstructural protein NSSB; parental sequence
OTHER INPORMATION: without cell culture-adaptive mutations
                                                                                                                                                                                                                                                                                                                                                                  Length 11076;
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                            FRATURE:
NAMB/KEY: CDS
LOCATION: (342)..(1193)
OTHER INFORMATION: hepatitis C virus core - neomycin oTHER INFORMATION: phosphotransferase fusion protein
                                                                                                        PEATURE:
NAME/KEY: RBS
LOCATION: (1202)..(1812)
OTHER INPORMATION: internal ribosome entry site from OTHER INPORMATION: encephalomyocarditis virus
                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.5%; Score 703.6; DB 4; Best Local Similarity 93.7%; Pred. No. 3.1e-176; Matches 733; Conservative 0; Mismatches 49;
LOCATION: (1)..(341)
OTHER INFORMATION: construct I389/Core-3'/wt
                                                                                                                                                                                                                                                                                                  ; NAME/KEY: 3.UTR
; LOCATION: (10846)..(11076)
US-09-539-601-1
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NAME/KEY: CDS
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   CTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG
                                                               GAGGACGCCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC
                                                                                                                                                                                          GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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APPLICATE BATCHING:
TITLE OF INVENTION: Hepatitis C Virus Cell Culture S
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT APPLICATION NUMBER: 199 15 178.4 GERMANY
RARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATCHING DATE: 2001.68-30
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09539601C Patent No. 6630343 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Hepatitis C
FEATURE:
NAME/KEY: 5'UTR
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TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
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NAME/KEY: CDS
LOCATION: (1342)..(1193)
OTHER INPORMATION: hepatitis C virus core - necomycin
OTHER INFORMATION: phosphotransferase fusion protein
PEATURE:
NAME/KEY: RBS
LOCATION: (1202)..(1812)
OTHER INFORMATION: internal ribosome entry site from
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LOCATION: (1)..(341)
OTHER INFORMATION: construct 1389/Core-3'/5.1
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ORGANISM: Hepatitis C virus
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US-09-539-601-25
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OTHER INFORMATION: hepatitis C virus polyprotein from core to OTHER INFORMATION: nonstructural protein NS5B; carries cell OTHER INFORMATION: culture-adaptive mutations from clone 9-13P
                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09539601C
Patent No. 6630343
GENERAL INFORMATION:
FALFILL INFORMATION:
FILE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REPERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
RAKLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
SARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
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NAME/KEY: CDS
LOCATION: (342)..(1193)
OTHER INFORMATION: hepatitis C virus core - neomycin
OTHER INFORMATION: phosphotransferase fusion protein
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NAME/KEY: RBS
NAME/KEY: RBS
OCHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
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Pred. No. 3.1e-176;
0; Mismatches 49;
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LOCATION: (1)..(341)
OTHER INFORMATION: construct I389/Core-3'/9-13F
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Best Local Similarity 93.7%;
Matches 733; Conservative
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; LOCATION: (10846)..(11076)
US-09-539-601-19
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US-09-539-601-19
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           PEATURE:
NAME/KEY: CDS
LOCATION: (1813)..(10845)
COTHER INFORMATION: hepatitis C virus polyprotein from core to OTHER INFORMATION: nonstructural protein NS5B; carries cell OTHER INFORMATION: culture-adaptive mutations of clone 5.1
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Pred. No. 3.1e-176;
0; Mismatches 49;
encephalomyocarditis virus
                                                                                                                                                                Query Match 88.5%;
Best Local Similarity 93.7%;
Matches 733; Conservative
                                                                                                            ; NAME/KEY: 3'UTR
; LOCATION: (10846)..(11076)
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 INFORMATION:
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NAME/KEY: 3'UTR
LOCATION: (10846)
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OTHER INFORMATION: hepatitis C virus polyprotein from core to OTHER INFORMATION: nonstructural protein NSSB; carries cell culture OTHER INFORMATION: adaptive mutations from clone no. 19
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                                                                   APPLICATE: Bartemachlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture
FILER REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
RARLIER APPLICATION NUMBER: 199 15 178-4 GERMANY
RARLIER APPLICATION NUMBER: 199 15 178-4 GERMANY
RARLIER PILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO
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                                                                                                      Culture
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OTHER INFORMATION: internal ribosome entry site
OTHER INFORMATION: encephalomyocarditis virus
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OTHER INFORMATION: construct 1389/Core-3'/19
Sequence 31, Application US/09539601C Patent No. 6630343 GENERAL INFORMATION:
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, NUMES/KEY: 3'UTR
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US-09-539-601-31
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ORGANISM: Hepatitis
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NAME/KEY: 5'UTR
LOCATION: (1)...(
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APPLICANT: OKAMOTO, Hiroaki
APPLICANT: NAKAMURIA, Tetsuo
TITLE OF INVENTION: OLIGONUCLECTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
TITLE OF INVENTION: HEPATITIS VIRUS
MUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young,
ADDRESSEE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
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TGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGCTAGCGTCCCCACTACGACGATA 2586
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONFURE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 16-UN-1995
RICH APPLICATION DATA:
APPLICATION NUMBER: JP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wellacher, Robert G
REGISTRATION NUMBER: 20,531
REFERRENCE/DOCKET NUMBER: 06/59-47083.1
TELECOMMUNICATION INPORMATION:
MATTORNEY/AGENT NUMBER: 06/59-47083.1
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/08470426B Patent No. 5856458 GENERAL INFORMATION:
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TELEPA:: (202) 659-146
INPERATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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                                                                                                         DB 2;
                                                                                                      Score 698.8; DB 2;
Pred. No. 3.1e-175;
0; Mismatches 52;
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                  TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                      Query Match
Best Local Similarity 93.4%;
Matches 730; Conservative
single
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STRANDEDNESS:
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  ; STRANDEDNES;
; TOPOLOGY: ;
; MOLECULE TYPE
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                                                                                                                                      544 GAGACGGTGCACGCACTGCTAATTTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
                                                                                                                                                             1219 GAGACAGTGCAGGACTGCAACTGCTCAATCTATCCCGGCCATTTATCAGGTCACCGCATG
                                                                                                                                                                                                                                            1279 GCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCCTAGTGGTGTGCGCGGTTGCTC
                                                                                                                                                                                                                                                                                                                                                                          664 CGGATCCCACACAAGCTGTCGTCGACATGGTCGTGGGGGGCCCCATTGGGGGAGTCCTGGCGGGT
                                                                GACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
                                                                                                                                                                                                                     GCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette, 5.25 inch, 360 Kb storage
COMPUTER: IRM AT competible
OPERATING SYSTEM: MS-DOS V3.2
SOFTWARE: WORDERFECT 5.0 (BOS text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/08191160
Fatent No. 6210675
GENERAL INFORMATION:
APPLICANT: Highlield, Peter Edmund
APPLICANT: Tedder, Brian Colin
APPLICANT: Tedder, Richard Seton
APPLICANT: Tedder, Richard Seton
APPLICANT: Barbara, John Anthony James
TITLE OF INVENTION: Viral Agent
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Rothwell, Figg, Ernst & Kurz
STREET: 1700 K Street
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/628,516
FILING DATE: 17 DEC 1990
APPLICATION NUMBER: 0K 92 8 562.1
FILING DATE: 18 DEC 1980
APPLICATION NUMBER: 0K 90 04 414.0
FILING DATE: 27 FEB 1990
PRIOR APPLICATION NUMBER: 0K 90 04 814.1
FILING DATE: 27 FEB 1990
FILING DATE: 27 FEB 1990
FILING DATE: 37 FEB 1990
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 27,195
REFERENCE/COCKET NUMBER: 1645-103A
RELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 833-5740
TELEFRAX: (202) 833-5744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: E. Anthony Figg
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GC 1460
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US-08-191-160-21
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    PRIMERS, AND THEIR HIGH-FIDELITY DETECTION OF NON-A, NON-B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   739 CTCGTCGGCGCCCCCTAGGGGGGCCTGCCAGGGCCTTGGCACACAGTGTCCGGGTTTCTG 798
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                      ADDRESSE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELB PC compatible
COREDATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN 1995
CLASSIPICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12 2-153402
FILING DATE: 12-JUN-1990
ATTOREY/AGERT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 698.8; DB 2;
Pred. No. 3.3e-175;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Wellacher, Robert G.
REGISTRATION NUMBER: 20,531
REBERENCE/DOCKET NUMBER: 06/59-47083.1
TELECOMOUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
TELEPAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: 14:
INFORMATION FOR SEQ ID NO: 14:
LENGTH: 1863 base pairs
  OLIGONUCLEOTIDE
APPLICATION FOR
HEPATITIS VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 93.4%;
Matches 730; Conservative
              TITLE OF INVENTION: APP
TITLE OF INVENTION: HEP
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge,
ADDRESSEE: L.L.F.
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SDNESS: single
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    TITLE OF INVENTION:
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STRANDEDNESS:
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69 CTTGTCGGCGCCCCCCTAGGGGGTGCTGCCAGGGCCCTGGCACATGGTGTCCGGGTTCTG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 TIGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 GGGATGTACCATGTCACGACGACTGCTCCAACTTCAAGCATTGTGTATGAGGCAGCGGAC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 ATGATCATGCATACCCCCGGGTGCCTGCGTTCGGGAGAACTACTCCTCCGTTGC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 resecrecercical contracted contracted and a second contracted can a second 
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                                                                                                                                                                                                                                       US-08-081-072-15
Sequence 15, Application US/08081072
Sequence 15, Application US/08081072
Sequence 15, Application US/08081072
GENERAL INFORMATION:
APPLICANT: NO. 56416540ru MAXI, Kenjiro YAMAGUCHI, Ayumi APPLICANT: TOYOSHIMA, and Michinori KOHAKA
TITLE OF INVENTION: NON-A NON-B HERPATITIS-SPECIFIC
TITLE OF INVENTION: DIAGNOSIS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-4280
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dike, Bronstein, Roberts & Cushman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh Classic
SOFTWARE: Microsoft Word Version 4.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,072
FILING DATE: June 22, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        932 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
                                                                                   ||
|1442 GC 1443
                                               785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                           784 GC
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                                           8 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: polyprotein
OTHER INFORMATION: viral structural and non-structural
OTHER INFORMATION: proteins
                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: from 308 to 2116 bp start of the PT-NANBH
                                                                                                                                                                                                                                                                                   PT-NANBH
                                                                                                                                                                                                                                                                                                                                                 LIBRARY: cDNA clones from 5' end of the genome
                                                         LENGTH: 2116 base pairs
TYPE: nucleotide with corresponding protein
STRANDEDNESS: single
                                                                                                                                                                                                                                                                               ORGANISM: human; serum infectious for
                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA to genomic RNA ORIGINAL SOURCE:
   21:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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US-08-449-093A-15
Sequence 15, Application US/08449093A
Sequence 15, Application US/08449093A
PEREDIX US. 5662906
TERREAL INFORMATION:
TITLE OF INVENTION: NON-A NON-B HERATITIS-SPECIFIC
TITLE OF INVENTION: ARTIGEN AND ITS USE IN HERATITIS
TITLE OF INVENTION: DIAGNOSIS
HUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STAKEB: AJON MILLS
CITY: MASSACHUSETTS
COUNTRY: USA
ZIP: O2109-4280
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,093A
FILING DATE: MAY 24, 1995
CLASSIFFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081,072
FILING DATE: June 22, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/726,141
FILING DATE: June 22, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOULOGY: linear
MOLECULE TYPE: CDNA to genomic RNA
US-08-449-093A-15
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   Length 932;
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87.5%; Score 695.6; DB 1;
llarity 93.1%; Pred. No. 1.8e-174;
Conservative 0; Mismatches 54;
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Query Match
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Matches 728; Conserv
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Copyright (c) 1993 - 2004 Compugen Ltd.
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June 16, 2004, 08:32:08; Search time 1473.55 Seconds (without alignments) 14206.949 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-899-303A-9 483 1 ATGCCCGGTTGCTCTTTCTC.....TGATGAACTGGTCCTAATAG Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3470272 seqs, 21671516995 residues Searched:

6940544 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmb]:* Database

em_un: *
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em_htgo_mus:* em_htgo_other:* em_htgo_hum: *

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

PAT 07-MAR-1997 1 (bases 1 to 483)
Maertens, G., Bosman, P., De, M.G. and Buyse, M.
Maertens, G., Bosman, P., De, M.G. and Buyse, M.
PURIPIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USB
Patent: WO 9604385-A 9 15-FEB-1996; linear DNA A48671 483 bp Sequence 9 from Patent WO9604385. A48671.1 GI:2302384 unidentified unidentified unclassified RESULT 1
A48671
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VERSION
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ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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240 300

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Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Plaviviridae;
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Purified hepatitis C virus envelope proteins for diagnostic and
therapeutic use
Patent: US 645503-A 9 12-JUN-2001;
Location/Qualifiers
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Location/Qualifiers
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1. .480
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Sequence 9 from Patent BP1211315.
AX452758 GI:21712443
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AR157327.1 GI:16218260
  INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304
Location/Qualifiers
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/product="unnamed"
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1 (bases 1 to 483)
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Purified Hepatitis C Virus envelope proteins for diagnostic
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                                                                                                                      Query Match
100.0%; Score 483; DB 6; Length 483;
Best Local Similarity 100.0%; Pred. No. 4.5e-113;
Matches 483; Conservative 0; Mismatches 0; Indels
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note="unnamed protein product"
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
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INNOGENETICS N.V. (BE)
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Sequence 9 from Patent WO02055548.
AX685010
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PCSAMYVGDLCGSVFLVSQLFTFSFRRHQTVQDCNCSIYPGHVSGHRNAMDMGNWS"
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Viruses; BSRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Purified Hepatitis C virus envelope proteins for diagnostic and
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    .480
    /note="unnamed protein product"

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Patent: WO 03051912-A 9 26-JUN-2003;
INNOGENETICS N.V. (BE)
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Sequence 9 from Patent WO03051912.
AX794852.
AX794852.1 GI:37515741
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/product="unnamed"
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Macrtens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
therapeutic use
Patent: US 6245503-A 11 12-JUN-2001;
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                                                                                                                   1. 480
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0; Mismatches 3;
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                            Other publication CA 2172273 960215
Other publication AU 3382495 960304.
Location/Qualifiers
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Sequence 11 from patent US 6245503.
AR157328 GI:16218261
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/product="unnamed"
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Best Local Similarity 99.4%;
Matches 476; Conservative
   INNOGENETICS NV
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ACCESSION
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Maertens,G., Bosman,F., De,M.G. and Buyse,M.
PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND
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/mol_type="unassigned DNA"
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WO9604385.
Location/Qualifiers
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/product="unnamed"
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A48673
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Best Local Similarity 100.0%;
Matches 483; Conservative 0
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/procein id="CAD86523.1"
/db_xxef="C1:29371418"
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/db_xxef="RMTRRMBL:CAD86523"
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VYEAADMIMHTPGGVPCVREGNSSRCWVALIPFLAARASVPTTIRRHVDLLVGAAA
PCSAMYGDLCGSVFLVSQLFTFSPRRHQTVQDCNCSIYPGHVSGHRMAWDMMNW"
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Hepatitis C virus
Virusee; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Maertens,G., Bosman,F. and Buyse,M.A.
Purified Hepatitis C Virus envelope proteins for diagnostic and
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                                                      Score 474.2; DB 6;
Pred. No. 8.1e-111;
0; Mismatches 3;
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/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"
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Patent: WO 02055548-A 11 18-JUL-2002;
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Sequence 11 from Patent WO02055548.
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Matches 476; Conservative
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/db_xxfef="G1:21712446"
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PCSAMYVGDLCGSVFLVSQLFTFSPRRHQTVQDCNCSIYPGHVSGHRWAWDMMNN"
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                                                                                 Length 480;
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                                                                                  Score 474.2; DB 6;
Pred. No. 8.1e-111;
0; Mismatches 3;
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/db_xref="taxon:11103"
Location/Qualifiers
1. .480
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/mol_type="unassigned DNA"
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/db xref="GI:37515744"
/tb xref="GI:37515744"
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Plaviviridae;
Hepacivirus.
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Purified Hepatitis C virus envelope proteins for diagnostic and
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                                Length 480;
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                                 DB 6;
                                 Score 474.2; DB 6;
Pred. No. 8.1e-111;
0; Mismatches 3;
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/mol_type="unassigned DNA"
/db_xref="taxon:11103"
/note="unnamed protein product"
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Patent: WO 03051912-A 11 26-JUN-2003;
INNOGENETICS N.V. (BB)
Location/Qualifiers
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/product="unnamed"
/product="unnamed"
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                                Query Match 98.2%;
Best Local Similarity 99.4%;
Matches 476; Conservative
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/noTe="isolated from a patient with liver cirrhosis and
hepatocellular carcinoma (HCC-5)"
                                                                                                                                                                                                                                                   241 AGGAACGCCACGCTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT
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Submitted (23-NOV-1999) Second Department of Internal Medicine,
Submitted (23-NOV-1999) Second Department of Internal Medicine,
Tokyo Medical and Dental University, 1-5-45 Yushima Bunkyo-ku,
Tokyo 113-8519, Japan
Location/Qualifiers
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Nagayama, K., Kurosaki, M., Enomoto, N., Miyasaka, Y., Izumi, N.
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  480;
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Hepatitis C virus strain MD25 complete genome.
AF207766
Score 474.2; DB 6;
Pred. No. 8.1e-111;
0; Mismatches 3;
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Hepacivirus.
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/organism="Hepatitis C virus"
/mol type="genomic RNA"
/strain="MD25"
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GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA

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242 1075 302

GGAACGCCAGCGTCCCCACTAAGACAATACGACGTCGACGTCGATTTGCTTGTTTGGGGCGG

GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCTG

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CHGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGCTTTTCCCTTGTTTCCC

AGCTGTTCACCTTCTCGCCCCCCCGCATGAGACGGTACAGGACTGCAATTGCTCAATTCT

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ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTC

AGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT

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DPPQPBYDLELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARSTPVNSWL
GNIMYAPTLWARMILMTHFPSTLLAQEQLEKNLDCQIYGACYSIEPLDLPQITQRLH
GLSÄFSLHSYSPGEINRVASCLRKLGVPPLRVWRLRARSVRAKLLSGGGRAATCGKYL
FNWAVETKLKLTPIPAASQLDLSNWFVAGYSGGDIYHSLSRARPRWFWLCLLLLSVGY
GIYLLPNR.
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WYRGDOLIWHTTCPCGAQITGHVKNGSWRIVDPRTCSWTWHGTPFVNATTGPCTPSP
APNYSKALWRYAABEYVEVTRYGDFHYVTGMTTDNVKCPCQVDAPEFFTRYDGYRLHR
YAPACKPLLREEVTFQVGLNQYLVGSQLPCEPBPDVAVLISMLTDPSHITAETAKREL
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VVSTLPQAVMGSSYGFQYSPGQRVEFLVNAWKSKRCPMGFSYDTRCFDSTVTENDIRT
BESIYQCCDLAPEARQAIRSLTBRLYVGGPLTNSKGQNCGYRRCRASGVLTTSCGNTL
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DHYRGVLKEIKAKASTVKAKLLSVEEACKLTPPHSARSKFGYGAKDVRNLSGKAVNHI
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KVVILDSFEPLRAEEBDEREVSVAAEVLRKSRKFPPALPIMARPDYNPPLLESWKDPDY
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translation="MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRI
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IREDATITIS C virus gene for structural protein, partial cds, isolate:HC-J4.
                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Nucleotide sequence of the genomic RNA of hepatitis C virus
isolated from a human carrier: comparison with reported isolates
for conserved and divergent regions
J. Gen. Virol. 72 (Pt 11), 2697-2704 (1991)
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Mink,M.A., Benichou,S., Madaule,P., Tiollais,P., Prince,A.M. and
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                                                                                                                                                                                                  Okamoto, H., Okada, S., Sugiyama, Y., Yotsumoto, S., Tanaka, T., Yoshizawa, H., Tsuda, F., Miyakawa, Y. and Mayumi, M. The S.-terminal sequence of the hepatitis C virus genome Upn. J. Exp. Med. 60 (3), 167-177 (1990)
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Analysis of the core and B1 envelope region sequences of variant of hepatitis C virus obtained in Indonesia
Arch. Virol. 136 (1-2), 53-62 (1994)
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Kawachi-gun, Tochigi-ken 329-04
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structural protein.
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Hepatitis C virus
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0; Mismatches 23; Indels
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Best Local Similarity 95.2%;
Matches 452; Conservative
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E04805 25-40 bp RNA linear PAT 29-SBP-1997 cDNA to 5'-terminal region of gRNA of Hepatitis nonA nonB virus.
E04805
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                                                                                                                                                                                                                                                                                                                                                                                                                   1. .2540
/note='a part of type non-A non-B hepatitis
HIGHLY SENSITIVE DETECTION METHOD OF NON-A NON-B TYPE HEPATITIS VIRUS USING OLIGONUCRECTIDE PRIMER AND OLIGONUCLECTIDE PRIMER PATEMIT: JP 1993023200-A 2 02-FEB-1993; MAKAWURA TETSUO PN JP 1993022200-A/2 PD 02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                             26-APR-1991 JP 1991191376
12-JUN-1990 JP 90P 153402
OXAMOTO HROAKI, NAKAMURA TETSUO
C12Q1/68,C12N15/51,C12Q1/70;
strandedness: Double;
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/organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic RNA
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               *source: strain=HC-J4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus,
                                                                                                                                                                                                                                                                         topology: Linear;
                                                                                                                                                                                                                                                                                             hypothetical: No:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E04805.1 GI:2173001
JP 1993091884-A/2.
unidentified
unidentified
                                                                                                                                                                                                                                                                                                                        anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
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ACCESSION
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B04805
                                                          JOURNAL
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          TITLE
                                                                                                       COMMENT
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                                                                                                                                                                                                                      /product="etructural protein"
/product="etructural protein"
/product="etructural protein"
/db_xref="G1:221514"
/db_xref="G1:221514"
/db_xref="G1:221514"
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GVRATRKTSERSQPRGWRQPIPKARRPEGRAMAQPGYPWPLYGNEGLGWAGNLLSPRG
GVRATRKTSERSQPRGWRQPIPKARRPEGRAMAQPGYPWPLYGNEGWAGNRULSPRG
GVRATGNLPGCSPFSIPLALLSCLTIPASAYEVRNVSGIYHTNDCSNSSIYTYLAD
GVNYATGNLPGCSPSIPLALLSCLTIPASAYEVRNVSGIYHTNDLLVGABAAFCSAMY
WGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHLSGHRMAWDMMCNWSPTTALVV
SQLLSIPQAVVDMVAGAHWGYLAGLAYYSWGNWAKVLIVALLFAGVDGETYTSGGAA
SHTTSTLASLFSPGASQRIQLVNTNGSWHINRTALNCNDSLHTGFLAALFYTHRFNSS
GCPERNASCRPIDWFAQGWGPITYTEPDSSPDQRPYCMHYAPRRFCGIVPASQVCGPVYC
FTPSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1146
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CDNA encoding a part of type non-A non-B hepatitis virus.
E04260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1027 GCGTTCGGGGAGACAACAGCTCCCGTTGCTGGGTAGCGCTCCACTCCCACGCTCGCGGCCA 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        847 TGCCCGGTTGCTCTTTCTCTTTGCTCTTTGCTGTCTGTGTTTGACCATCCCAG 906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.1%; Score 435; DB 14; Length 1880;
.larity 94.7%; Pred. No. 9.1e-101;
Conservative 0; Mismatches 25; Indels 0
                                                                                                       /db_xref="taxon:11103"
/note="82 bp upstream of StyI site"
                                   'organism="Hepatitis C virus"
'mol type="genomic RNA"
'isolate="HC-J4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 2540)
Okamoto, H. and Nakamura, T.
                                                                                                                                                                              /note="putative"
/codon_start=1
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JP 1993023200-A/2.
unidentified
unidentified
unclassified.
                                                                                                                                                         342. .>1880
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E04260
LOCUS
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181

996

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Gaps

1086

301

361

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10-MAY-1994
20-JUN-1991 JP 1991247120
OKAMOTO HIROAKI, NAKAMURA TETSUO
C12N15/51,C12N1/21,C12P21/02,C12Q1/70,G01N33/53,G01N33/569, PC
                                            SM unidentified
unclassified.
Uclassified.

B 1 (bases 1 to 2540)
S Okamoto, H. and Nakamura, T.
OLICONUCLEROTIDE PRIMER AND METHOD FOR DETECTING NON-A AND NON-B
TYPE HEAPITIS VIRUS IN HIGH SENSITIVITY
Datent: JP 1994125777-A 4 10-MAY-1994;
NAKAMURA TETSUO
PN JP 1994125777-A/4
PD 10-MAX-1994
PP 20-JUN-1991 JP 1991247120
PI OKAMOTO HIROAKI, NAKAMURA TETSUO
PC CLOMIS/51,C12N1/21,C12P21/02,C12Q1/70,G01N33/53,G01N33/569, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 AGCTGTTCACCTTCACCTCGCCGGCATCAAACAGTACAGGACTGCCAACTGCTCAATCT
                                                                                                                                                                                                                                                                                                       /organism='Hepatitis non-A non-B virus'/strain='He-014'
1. .341
ide 342. .1490
/note='non-structural protein of chimpar
hepatitis non-A
                                                                                                                                                                                                                                                                                                                                                                                                                   chimpanzee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2540;
                                                                                                                                                                                                                                                                                                                                                                                                                   protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IndelB
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                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  'note='Structural
                                                                                                                                                                                                                                                                                                                                                                                                                                          non-B virus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .2540
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                         1491. .2540
                                                                                                                                                                                                                                                                                                                                                                                                                                hepatitis non-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                              strandedness: Single;
                                                                                                                                                                                                                                            topology: Linear;
hypothetical: No;
            B07391.1 GI:2175530
JP 1994125777-A/4.
                                                                                                                                                                                                                                                                    anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                  unidentified
                                                                                                                                                                                                                    G01N33/576;
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   CIGCITICIGCICCCGCTATGTACGTGGGGGGATCTCTGCGGGATCTTTTCCTCGTCTCCCC 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCCGGTTGCTCTTTCTCTTCCTTCTTGCTTTGCTGTCCTGTTTGACCATCCCAG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTGTTCACCTTCACCTCGCCGCATCAACAGTACAGGACTGCAACTGCTCAATCT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                          Score 435; DB 6; Length 2540;
Pred. No. 9.2e-101;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               807391 2540 bp RNA linear P CDNA encoding chimpanzee hepatitis non-A non-B virus.
                                                                                                                                                                                                                                                      R 1. .341
342. .2540
/note='protein virus gene'.
Location/Qualifiers

    .2540
    /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                                                                                                                          90.18;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94.7
Matches 450; Conservative
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Search completed: June 16, 2004, 11:39:17 Job time : 1474.55 sec8

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GenCore version 5.1.6
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June 16, 2004, 07:39:53; Search time 181.729 Seconds (without alignments) 11290.892 Million cell updates/sec Run on:

US-09-899-303A-9

Perfect score:

1 ATGCCCGGTTGCTCTTTCTC.....TGATGAACTGGTCCTAATAG 483 Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

3373863 seqs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

N Geneseq 29Jan04:* Database :

geneseqn2003bs:*geneseqn2003cs:* geneseqn2001as:*geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn1990s:* geneseqn2000s:* 4.2.0.2.8.9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

	Description	Aat12707 HCV B1 CO	Aal48916 Hepatitis	Add55517 Hepatitis	Aat12708 HCV B1 co	Aal48917 Hepatitis	Add55519 Hepatitis	Aag24467 NANB hepa	Aba03491 Cuticle p	Aaq43889 NANB hepa	Aaq63753 NANBHV ge	Aaq15363 Fragment	Aag29628 Hepatitis		Aaf23492 Infection	Aac86939 Nucleotid	Aax24833 Infection	Aag35081 HCV envel	Aba03492 Cuticle p	Aag11076 Fragment	Aa207647 HCV J1 B	Aag35085 HCV envel	Aaq79750 Hepatitis	Aax00401 Hepatitis
	ID	AAT12707	AAL48916	ADD55517	AAT12708	AAL48917	ADD55519	AAQ24467	ABA03491	AAQ43889	AAQ63753	AAQ15363	AAQ29628	AAX24843	AAF23492	AAC86939	AAX24833	AAQ35081	ABA03492	AAQ11076	AAZ07647	AAQ35085	AAQ79750	AAX00401
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	Score	483	483	483	474.2	474.2	474.2	435	435	435	435	433.4	431.8	430.2	430.2	430.2	430.2	428.6	428.6	425.8	425.8	425.4	425.4	425.4
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Aax26733 Consensus	Aax26728 Consensus	Aaq79772 Hepatitis	Aax26739 Consensus		Aal55222 Plasmid p	Aav60673 Pragment	Aag64069 Non-A, no	Aat30387 5'UTR/COR	Aaq64068 Non-A, no	Aat30386 5'UTR/COR	Aag27160 NANB hepa	Aat12704 HCV B1 co	Aal48913 Hepatitis	Add55634 Hepatitis	Aav60668 Fragment	Aaq35086 HCV envel	Aag79758 Hepatitis	Aaq79760 Hepatitis	Aaq79759 Hepatitis	Aat12705 HCV B1 co	Aal48914 Hepatitis
AAX26733	AAX26728	AAQ79772	AAX26739	AAV60672	AAL55222	AAV60673	AAQ64069	AAT30387	AAQ64068	AAT30386	AAQ27160	AAT12704	AAL48913	ADD55634	AAV60668	AAQ35086	AAQ79758	AAQ79760	AAQ79759	AAT12705	AAL48914
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24	25	56	27	28	29	30	. 31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAT12707 standard; DNA; 483 BP 23-SEP-1996 (first entry) HCV El construct HCCI12A. AAT12707; RESULT 1 AAT1270

HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;

Hepatitis C virus.

WO9604385-A2

15-FEB-1996.

95WO-EP003031. 31-JUL-1995;

94BP-00870132. 29-JUL-1994;

(INNO-) INNOGENETICS NV.

Buyse M; De Martynoff G, Bosman F, Maertens G,

WPI; 1996-129401/13.

Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.

Claim 23; Fig 21; 146pp; English.

and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1

30-AUG-2001; 2001US-0315768P

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serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed BI. R2 and BI/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
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                                                                                                                                                                                                                         Sequence 483 BP; 85 A; 152 C; 123 G; 123 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                           New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AGGAACGCCAGCGTCCCCACAACAACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCT
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100.0%; Pred. No. 3.9e-131;
ive 0; Mismatches 0;
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Matches 483; Conservative
                                                                                                                      Bosman F,
                                                           (INNO-) INNOGENETICS
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AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) El and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant B1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating bumans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed BL, E2 and BL/E2, and claiminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.
     361 CAGCTGTTCACCTTCTCACCTCGCCGCATCAAACAGTACAGGACTGCAACTGCTCAATC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera:
                                                                             1 ATGCCCGGTTGCTCTTTCTCTTTCTCTTTGGCCCTGCTGTCCTGTCTGACCATACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23; Fig 21; 146pp; English.
                                                                                                                                                                                                                                                                                                                                    AAT12708 standard; DNA; 480 BP.
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Best Local Similarity
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                                                                                                                                                                                                                               C virus; HCV; vaccine; liver disease; El protein; E2 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver disease. The vaccine of the invention comprises an HCV El or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present DNA sequence encodes an HCV El more in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTCCGCTTATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAAGGACTGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patitis C virus (HCV) vaccine composition, useful for reducing disease, e.g., liver fibrosis in a chronic HCV-infected mammal
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100.0%; Pred. No. 3.9e-131;
iive 0; Mismatches 0;
                                                                                                                                                                               Hepatitis C virus Bl protein coding sequence #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bosman F;
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16-OCT-2002; 2002US-0418358P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2002; 2002WO-EP014480
                             ADD55517 standard; DNA; 483
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                                                                                                                               (first entry)
                                                                                                                                                                                                                                                            liver fibrosis; ds; gene.
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                                                                                                                                                                                                                                  Hepatitis
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                                      TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCCTA
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virucide; immunostimulant; vaccine; ds.
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an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV E3 and/or E2 proteins are useful as vaccines or therespeutics, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention
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Pred. No. 1.5e-128;
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16-OCT-2002; 2002US-0418358P.
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Best Local Similarity 99.49
Matches 476; Conservative
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                                                                                                                                                                                                                                                                                                                                    Recombinant cDNA of NANBH virus strain HC-JS and corresp. peptides -
useful for diagnosis and in vaccines and immunological pharmaceuticals.
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90.1%; Score 435; DB 2;
Best Local Similarity 94.7%; Pred. No. 7e-117;
Matches 450; Conservative 0; Mismatches 25
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P-PSDB; AAR24087.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTCCGGTTGCTCTTTCTCTTTCCTCTTGGCCCTGCTGTCCTGTCTGACCATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGTTCGGGAGGCAACTCCTCCGGTTGCTGGGTGGCGCTCACTCCCCACGCTCGCGGCC
                                                                                                                                                                                       The invention comprises an Hepatitis C virus (HCV) vaccine for reducin liver disease. The vaccine of the invention comprises an HCV B1 or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                  hepatitis C virus (HCV) vaccine composition, useful for reducing
or disease, e.g., liver fibrosis in a chronic HCV-infected mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-A, non-B hepatitis virus; NANBHV; PCR;
amplification polymerase chain reaction; vaccine; antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                      Length 480;
                                                                                                                                                                                                                                                                                                 Sequence 480 BP; 85 A; 149 C; 123 G; 123 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                  Score 474.2; DB 9;
Pred. No. 1.5e-128;
0; Mismatches 3;
                                                                                                                                                                                                                                                                present DNA sequence encodes an HCV El protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NANB hepatitis virus strain HC-J4 genome
                                                                                                                                                        Example 1; SEQ ID NO 11; 271pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                Ë
                  Bosman
                                                                                                                                                                                                                                                                                                                                Query Match 98.2%;
Best Local Similarity 99.4%;
Matches 476; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ24467 standard; DNA; 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-A.
non-B hepatitis virus.
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                                                 2003-541632/51
                                                                   P-PSDB; ADD55520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen related to non-A and non-B hepatitis virus - comprises non-
translation region comprising 340 - 341 mols. of nucleotides, non-
translation region comprising 1885 - 2551 mols. of nucleotides including
region 1,149 and, etc.
                          AGCTGTTCACCTTCTCGCCTCGCCGCATGAGACAGTGCCAGGACTGCAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 recognificating transfer contrades constructed and a recognification of the second s
AGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-A, non-B; virus; polymerase chain reaction; detection; sensitive; specific; HCV; NANEH; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                           ATCCCGGCCATGPATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTC 476
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Pred. No. 7.8e-117;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5' terminal of NANBH virus RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2540 BP; 471 A; 775 C; 741 G; 553 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 NANB hepatitis virus polymucleotide N-2540-2
                                                                                                                                                                                                                                                                              AAQ43889 standard; cDNA to mRNA; 2540 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 19-20; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/note= "from 5
342. .2540
/*tag= a
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Best Local Similarity 94.7%;
Matches 450; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-A.
non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-199637/25.
P-PSDB; AAR38279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP05091884-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                              21-0CT-1993
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                                                                                                                                                                                                                                                                                                                                 AAQ43889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNGCTTTCTGTTCCGCTATGTACGTGGGGAATCTCTGCGGAATCTGTTTTCCTTGTTTTCCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGTTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to cuticle protein 1 and 2 secreting hepatitis C virus. The present sequence is a coding sequence provided in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                           Cuticle protein 1 and 2 secreting hepatitis C virus related DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cuticle protein 1 and 2 secreting hepatitis C virus (Japanese)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2187;
                                                                                                                                                                                                                              Cuticle protein 1; cuticle protein 2; hepatitis C virus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2187 BP; 406 A; 669 C; 631 G; 481 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /partial
/note= "no stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                            "AAM47264"
                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 2-4; 7pp; Korean.
                          ABA03491 standard; DNA; 2187 BP.
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/product= '
                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-1996;
                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                        15-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-0CT-1997.
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1207 AGCTGTTCACCTTCTCGCCTCGCCATGAGACAGTGCAGGACTGCAACTGCTCAATCT 1266
                                                                                                                                                                        1027 GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGGCCA 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligo-nucleotide primers - derived from and used to detect and diagnose non-A , non-B hepatitis virus.
                                                                                                                                                                                                                              GGAACGCCAGGCTCCCCACAACGACGACTACGACCCCACGTCGATTTGCTCGTTGGGGCTG
                                           GCGTTCGGGAGGCCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                                                                                                                                                                       CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGCGCATCTGTTTTCCTTGTTTTCCC
                                                                                                                                                                                                                                                                                                                             AGCTGTTCACCTTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                 Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                    ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pragment of NANB hepatitis virus strain HC-J4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus.
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17-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer pairs specific for non-A, non-B hepatitis virus used for high sensitivity detection of non-A non-B (NANB) hepatitis
             GGAATGCCAGCGTCCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGGCGG
                                                                                                                                                                                                                                                         GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                          GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymerase chain reaction; PCR; primer; amplify; detection; NANBHV; non-B hepatitis virus; 5'-terminal region; core protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.1%; Score 435; DB 2; Length 25 Best Local Similarity 94.7%; Pred. No. 7.8e-117; Matches 450; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                AAQ63753 standard; cDNA to mRNA; 2540 BP
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RESULT 10 AAQ63753 ID AAQ6

Claim 1; Page 7; 23pp; English

2 TGCCCGGTTGCTCTTTCTTTCCTCTTGGCCCTGCTGTCCTGTCTGACCATACCAG 61

91JP-00191376

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26-APR-1991;
                                                                                     Detection of primers with
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                                            Okamoto H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTGTTCACCTTCTCGCCTGGCCGGCATGAGACAGTGCAGGACTGCAAGTGCTCAATCT 1249
         NANB hepatitis virus strain HC-J4 was isolated from a plasma sample of a chimpanzee challenged with NANB hepatitis for infectivity but which tested negative for HCV antibody by Ortho HCV Ab ELISA test. RNA was isolated from the sample and reverse transcribed into cDNA. The 513 amino acids encoded by the CDS were determined but are not given in the specification (and hence are not included in A-Geneseq). A study of the deduced sequence suggested that the CDS encodes NANBH virus core proteins. Friners for detecting NANB hepatitis virus were designed based (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                         CTGCTTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCCC
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                                                                                                                                                  / Match 89.7%; Score 433.4; DB 2; Length 1863; Local Similarity 94.5%; Pred. No. 2.1e-116; nes 449; Conservative 0; Mismatches 26; Indels 0;
                                                                                                                                Sequence 1863 BP; 333 A; 586 C; 547 G; 397 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus HC-J4 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
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16-MAR-1993
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                                                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                          This sequence represents the 5' region of hepatitis C virus RNA. The original sample was obtained from human and chimpanzee plasma. RNA was isolated from several samples and homology compared, and the respective sequence of about 1900 - 2500 nucleotides of the 5' terminus and 1100 nucleotides of the 3' terminus determined. The 5' region (given) contains a non-coding region of at least 340 nucleotides and a region coding for the beructural protein followed by a region coding for the non-structural protein followed by a region coding for the non-structural protein (none actually detailed on the sequence given in the specification). When compared with the sequence of HCV disclosed in EP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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                                                                                                                                                    non-A, non-B hepatitis virus - using new oligo-nucleotide nucleotide sequences corresp. to part. of the viral RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1027 GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAATGCCAGGTCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGTTCGGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAACGCCAGCCTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCCGGTTGCTCTTTCTCTTTCTTTGGCCCTTGCTGTCTGTCTGACCATACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2540 BP; 472 A; 775 C; 741 G; 552 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 431.8; DB 2; Length
Pred. No. 6.7e-116;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                    Disclosure; Page 18; 54pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 94.3
Matches 448; Conservative
(IMMO ) IMMUNO JAPAN INC
                                                    Nakamura
                                                                                                     WPI; 1992-359137/44
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                 HCV; infectious clone; infection; diagnosis; therapy; vaccine; screening; assay; antiviral; virucide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated hepatitis C virus nucleic acids - used to develop products for the diagnosis, prevention and treatment of HCV infections and for developing screening assays.
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Pred. No. 3.2e-115;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                            Emerson SU, Purcell RH;
                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                Location/Qualifiers
342. .9374
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 14A-F; 126pp; English
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98US-00014416.
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94.18;
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Best Local Similarity 94.1;
Matches 447; Conservative
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P-PSDB; AAW98022.
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                                                                  Hepatitis C virus.
                                                                                                                                                                                                                                      16-JUL-1998;
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GGAATGCCAGCGCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGACGG 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to GB virus-B. The nucleic acid molecules of the invention are useful for indirectly studying the molecular properties of hepatitis C virus (HCV). The infectious nucleic acid sequence of the GB virus-B clone and the HCV/GBV-B chimeras may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New infectious nucleic acids of the GB virus-B clone, useful for indirectly studying the molecular properties of hepatitis C virus (HCV) and in developing vaccines and therapeutics for HCV.
                                                                                                                                                                                                                                CTGCTTTCTGCTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTATTTTCCTCGTCTCCCC
                                                                                                                                                                                                                                                                                                                                                CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTTCCC
                                                                                                                                                                                                                                                                                                             AGCTGTTCTCTCTCTCCCCCCCCCCCAACACAGTACAGGACTGCAACTGCTCAATCT
                                                                                  GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGATGACTGGTC 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infectious Hepatitis C virus 1b genotype.
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Best Local Similarity 94.1
Matches 447; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid comprising a chimeric bovine viral diarrhea virus genome in which the (non-)structural region has been replaced by hepatitis C virus (HCV) genome useful for treating or preventing HCV signs and
                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric virus; bovine viral diarrhoea virus; BVDV; hepatitis C virus;
                                                         GTGTTCAGGAGGGTAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGGCA
                                                                                                   GGAATGCCAGCGTCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGACGG
                                                                                                                                                                                               AGCTGTTCACCTTCTCGCCCTCGCCAGCATGAGACAGTGCAGGACTGCAACTCCTCAATCT
                     GCGTTCGGGAGGCCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCCACGCTCGCGGCCA
                                                                                       GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a hepatitis C virus (HCV) clone genotype 1b.
                                                                                                                                                                                                                                                                                                                                                                                                                     HCV; vaccine; viral inhibitor; antiviral; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purcell RH;
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The specification describes a nucleic acid comprising a chimeric virus genome, specifically bovine viral diarrhoea virus (BVDV) genome in which the (non-) structural region has been replaced by the (non-) structural region of a hepatitis C virus (HCV) genome. The nucleic acids comprising the chimeric virus and the chimeric virus are useful for identifying cell lines capable of supporting the replication of these chimeric viruses, in

Disclosure, Fig 4A-F; 97pp, English.

symptoms

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creening for neutralizing antibodies to HCV of different genotypes, in the production of HCV-BVDV virions, for the development of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, in studying the molecular properties of HCV indirectly in virro, and in identifying inhibitors of viral enzyme activity which would be useful as antiviral agents. Formulations or compositions comprising the chimeric virions may be used to treat or prevent the signs and symptoms of HCV. The present sequence represents a HCV clone, which is used to construct chimeric nucleic acids of the invention
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                                                                                                                                              Sequence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 U; 0 Other;
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                                                                                                                                                                           4; Length 9595;
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                                                                                                                                                                        Score 430.2; DB 4;
Pred. No. 3.2e-115;
0; Mismatches 28;
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Best Local Similarity 94.1%;
Matches 447; Conservative (
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AVG3335 AVG38120
CCG34833 OGCCB40TH
EX421743 BX421743
ALG5598 AL565958
CCG34833 OGCBG10
AVG33658 AVG3658
CCG34434 OGUFC24TV
BZ557931 msh2 5817
CCC344434 OGUFC24TH
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EI098866 IP1_34_C0
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1 (bases 1 to 48)

2 (bu, J. Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H., Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zang, Liu, R., Jia, J., Fu, G., Ren, S., Zhong, M., Cheng, Z., Xu, Z., Gu, W., Jia, J., Fu, G., Ren, S., Zhong, M., Chen, Z., Chen, S., Han, Z. and Chen, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Zeguang Han
Si Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Trel: 86-21-50801919 (ex. 45)
Pax: 86-21-50801922
Bmail: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV755731 AV Homo Bapiens CDNA clone BMPAKB03 5', mRNA sequence.
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   CG300832
CG213867
CC634840
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CD206870
CB924688
AV633658
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AV755731.1 GI:10913579
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39.2
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VERSION
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DEFINITION
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AV758366 AV758366
CP946043 psHB036xB
BZ645446 OGCBJ86TC
                                                                                                      June 16, 2004, 09:12:53; Search time 1298.46 Seconds (without alignments) 11108.065 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                               1 ATGCCCGGTTGCTCTTTCTC.....TGATGAACTGGTCCTAATAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                    55026578
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                       27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               nucleic search, using sw model
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AV758366
CF846043
BZ645446
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Gapop 10.0 , Gapext 1.0
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em esthum: *
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em gss vrl:*
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Maximum DB seq length: 200000000
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em_gas_f
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534
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11.5
8.9
8.6
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55.6
43.2
41.6
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Perfect score:
                                                                                                                                                                                                                             Scoring table:
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PEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 TCTGTTCCGCTATGTACGTGGGGATCTCTGTTTTTCCTTGTTTTCCCAGCTGT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 racescerececeantracerarcecareeerrceceerresecricaacaacreeace 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 TCGATGGACCAGAAGAAGAGCCCCGATCATGCTGACCCCCAAGACGGTGGCCAACATTCAC 319
                                                                                                                                                                                               457 rerearcaecreacracererresacerereseerraceserraceserreseereaces
                                                                                                                                                                                                                                                           368 TCACCTICTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCTATCCCG 427
                                                                                                                                                                                                                                                                                                 397 TTA---TCTCTCAGCAGGAAGCATTGGTTTGTGCAAGAGAATGCAACTGCTCATTCTATCCTG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="mycelium"
/cell line="P6497"
/dev stage="48 hr. post infection stage"
/lab_bost="Soybean plant"
/clone lib="WJSDA-IRAES: Expression of Phytophthora sojae
genes during infection and propagation_SHB"
/note="Vector: pBK-CMV; Site_1: EcoRl; Site_2: Xhol"
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytophthora sojae
Bukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
Phytophthora.
                                                                                                                                                                                                                                                                                                                                                                                  428 GCCATGTATCAGGTC-ACCGCATGGCTTGGGATATGATGATGAACTGGTC 476
                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                  340 GCTGCATCACTGGACTACAGTATGGCTATGATGATGAACTGGTC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%; Score 43.2; DB 14; Length 534; 47.4%; Pred. No. 3.4; tive 0; Mismatches 143; Indels 0.
                         Length 492;
                  Query Match 11.5%; Score 55.6; DB 9; Length 4 Best Local Similarity 65.9%; Pred. No. 0.0024; Matches 112; Conservative 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Bamil: bmtyler@vt.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 534.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: BK reverse primer BACKWARD: BK reverse primer Place: 036 row: B column: 09 Seq primer: BK reverse primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="sHB036B09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF846043.1 GI:38061697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tyler, B.
Tyler, B. Not Published
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 534)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Tyler B
Tyler lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .534
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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CF846043
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[Ubase] Ito 4913

[Ubase] Ito 492

[Ubase] Ito 493

[Ubase] Ito 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 GPTGGGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGCAGTTCAGCTGATCA---TCTGGCCTCAGCACCATGAGTTTGTGCATGAATGCAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 CITIGETTICCCAGCEGETGTECACCTTCACCTCGCCGGCATCAAACAGTACAGGACTGCAAC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zeguing Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Bmail: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Bone marrow"
/cell type="CD34+ hematopoletic stem/progenitor cell"
/lab_bolt="BM25.8"
/clone_lib="BM75.8"
/note="Vector: pTriplBx2; Site_1: sfilA; Site_2: sfilB"
                                                                                                                                                                /tissue_type="Bone marrow"
/cell type="CD34+ hematopoietic stem/progenitor cell"
/lab_fost="BMA5.8"
/clone_lib="BM"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV758366 BM Homo sapiens cDNA clone BMPAKA03 5', mRNA sequence.
AV758366 BM Homo sapiens cDNA clone BMPAKA03 5', mRNA sequence.
AV758366
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                  13.9%; Score 67.2; DB 9; Length 488; 67.0%; Pred. No. 2.8e-06; Live 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                     'organism="Homo sapiens"
                                                                                 mol_type="mRNA"
|db_xref="taxon:9606"
|clone="BMPAKB03"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens cDNA BM clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="BMFAKA03"
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 67.09
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLII | CTGGTCGT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGTCCT 478
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KEYWORDS
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AV758366/c
LOCUS
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CG213867 1.5_KB Zea mays genomic clone ZMMEMa0506110,
                                                                                CG300832 A1 bp DNA linear GSS 25-AUG-2003 OGWJO73TV ZM 0.7_1.5_KB Zea mays genomic clone ZMMEMa0603M01, genomic survey sequence.
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Exkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Exkaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (Dases I to 741)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Consortium for Manize Genomics
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSs: OGCB1367M
Contact: Cathy Whitelaw
GAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCAGGAACGCC
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/clone lib="zm0.7 1.5 XB"
/note="vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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ive 0; Mismatches 99; Indels 0;
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Fax: 301-838-0208
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(Dases 1 to 761)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Kesnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
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/clone="ZWRBWa0500508"
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50.5%; Pred. No. 11;
ive 0; Mismatches
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/mol_type="genomic DNA"
/strain="B73"
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/strain="B73"
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/clone="ZMMBMa0723H15"
                            Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: Sheared ends.
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Contact: Cathy Whitelaw
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Matches 101; Conservative
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Fax: 301-838-0208
            Tel: 301-838-5843
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1 (bases 1 to 995)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Citek, R.W., Robbins, D. and Lakey, N.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 794)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Fraeer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSs: OGVCR5JH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 ceracchecegrescencerceaceandanasias de consecencementados de 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4577"
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/clone=lib="zw_0.71.5_KB"
/note="Vector: pBGSK-; Site 1: HinclI; 0.7-1.5 kb
methylation filtered genomic DNA library"
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llarity 50.5%; Pred. No. 10;
Conservative 0; Mismatches 99;
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/strain="B73"
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                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Other_GSSs: OGVCB40TH
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Class: sheared
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Contact: Erika Asamizu
Contact: Rrika Asamizu
The First Laboratory for Plant Gene Research
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3 Kisarzu, Chiba 292-0812, Japan
Bmail: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

Location/Qualifiers

1. 399
(organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/gtrain="C9"
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/clone="HC097407_r"
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Chlamydomonas reinhardtii
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Chlamydomonadaceae, Chlamydomonas.

Chlamydomonadaceae, Chlamydomonas.

Raamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.

Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii

DNA Res. 7 (5), 305-307 (2000)
CGGGGTGTACCATGTCACGACGGCTCCCAACTCAAGCATAGTGTATGAGGCAGCGGA
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                                                                                                                                                                                                                                                                                                                                                                                   AV638521 399 bp mRNA AV638521 Chlamydomonas reinhardtii 5% CO2 CDNA clone HC087407_r 5', mRNA sequence. AV638521
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Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                   41 TGFCCTGTCTGACCATACCAGCTTCCGCTTATGAAGTGCGCAACGTGTCCGGGGGTGTACC 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 CCAACTCGCAGTCGTTCGCCAACACCGGCGCGCTGGTGACCTGCGTCAAGAACTTCCCCG 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
1 (bases 1 to 526)
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    /clone lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic_DNA library"
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                                                                                                                                                                                              DB 29; Length 761;
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/clone="A09_p234_plate_14"
/tissue_type="drought stressed seedlings"
/dev_stage="21 days old"
/clone_lib="p:234"
                                                                                                                                                                                         Score 40.8; DB 29; Length
Pred. No. 16;
0; Mismatches 147; Indels
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Long Ashton, Bristol BS41 9AF United Kingdom.
Location/Qualifiers
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/cultivar="mercia"
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Best Local Similarity 57.55
Matches 73; Conservative
                                                                                                                                                                                                                                                                      Matches 129; Conservative
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/strain="C9"
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                                                                                                                                                                                                                                                         Contact: Brika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3055"
-[clone="http://dr.074a01 r"
/clone lib="Chladronnas reinhardtii 5% CO2"
/note="vector: pBluescriptII SK-; Site_1: BcoRI; Site_2:
/khoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
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    (bases 1 to 440)
    Asamizu, B., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.

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Chlamydomonas rainhardtii
Eukaryota, Viridiplantee; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                               Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                 1 (bases 1 to 434)
Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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DNA Res. 7 (5), 305-307 (2000)
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1 Similarity 51.4%; Pred. No. 18;
93; Conservative 0; Mismatches 88; Indele
                                                                                                                                                                                                                                                                                                                                                                       /organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/etrain="C9"
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Contact: Erika Agamizu

Contact: Erika Agamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisazuzu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

Email: acation/Qualifiers
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Contact: Brika Asamizu
The First Laboratory for Plant Gene Research
Karusa DNA Research Institute
Karusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonadaceae; Chlamydomonas.
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/clone="HC080c04_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
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/mol type="RNNA"
/strain="C9"
/db_xref="taxon:3055"
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/clone="Hc071f12 r"
/clone=lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescript1 SK-; Site 1: BcoR1; Site 2:
Xho1; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
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             /clone_lib="Chlamydomonas reinhardtii 5* CO2" hote="Vector: pBluescriptil SK-; Site 1: BcoRI; Site_2: Xho1; The CDNA library was constructed from cells cultured in a medium with bubbling air containing 5* carbon
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Chlamydomonadaceae; Chlamydomonas.
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Nakamuza, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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/mol_type="mRNA"
/strain="C9"
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Pred. No. 18;
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/clone="HC070g06 r"
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l Similarity 51.4%;
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/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed_from cells cultured
in a medium with bubbling air containing 5% carbon
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Bmail: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Chlamydomonas reinhardtii
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Chlamydomonas reinhardtii
Chlamydomonadaceae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonae.

1 (bases 1 to 451)
Asamizu, B., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamizu, B., Miura, K., Gucho, E., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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150 CATGATCATGCACACCCCGGGGGGGGCGTTCGGGTTCGGGAGGGGAAGTCCTCCCGTTG
                                                                                        CGGGGTGTACCATGTCACGAACGACTCCCAACTCAAGCATAGTGTATGAGGCAGCGGA
                                                                                                                                              CATGATCATGCACCCCCCGGGTGCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Chlamydomonas reinhardtii"
|mol_type="menNA"
|strain="C9"
|db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV637643 AV637643 Chlamydomonas reinhardtii 5% CO2 CDNA clone HC075903_r 5', mRNA sequence.
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51.4%; Pred. No. 18;
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376 C 376

Search completed: June 16, 2004, 13:27:13 Job time : 1300.46 secs

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FRATURE:
NAME/KEY: mat_peptide
LOCATION: 1..477
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4
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Sequence 30, Appl
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Sequence 5, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 49, Appli
Sequence 49, Appli
Sequence 7, Appli
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Sequence 11, Appli
Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 14, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 96, Appli
                                                               June 16, 2004, 09:14:33 ; Search time 34.8162 Seconds (without alignments) 7698.741 Million cell updates/sec
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Sequence 7, Al
Sequence 13, 1
Sequence 13, 1
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1 ATGCCCGGTTGCTCTTTCTC.....TGATGAACTGGTCCTAATAG 483
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(cgn2_6/ptodata/2/ina/5A_COMB.eeq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/epcTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-927-597-11

US-08-927-597-11

US-08-470-4268-17

US-09-014-416-4

US-09-014-416-6

US-09-1014-416-6

US-08-15-2048-96

US-08-483-695-30

US-08-483-695-30

US-08-483-695-30

US-08-612-973-3

US-08-612-973-3

US-08-612-973-47

US-08-612-973-47

US-08-612-973-7

US-08-612-973-7

US-08-612-973-7

US-08-612-973-7

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                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                               682709 segs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
                                                                                                                                                 IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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No.
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28 422.2 | Sequence 1, Appl. 29 | Sequence 1, Appl. 20 | Sequence 2, Appl. 20 | Sequence 3, Appl. 20 | Sequence 3,
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TGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCC 240
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Best Local Similarity 100.0%; Pred. No. 7.5e-128;
Matches 483; Conservative 0; Mismatches 0;
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Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MARKTENS, GERT
APPLICANT: BOSMAN, FONS
PILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFREENCE/DOCKET NUMBER: 1487-
TELECOMMUNICATION INFORMATION:
TELEPONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat_peptide
LOCATION: 1..477
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FEATURE:
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US-08-612-973-11
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                                                                     Gaps
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TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
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                                    Length 483;
                                100.0%; Score 483; DB 3; Length 4
100.0%; Pred. No. 7.5e-128;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version
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CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 9, Application US/08927597; Patent No. 6245503; GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT APPLICANT: BOSNAN, FONS APPLICANT: DE MARTYNOPP, GUY; APPLICANT: BUYSE, MARIE-ANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DA
                               Query Match
Best Local Similarity 100.4
Matches 483; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON STATE: VIRGINIA
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   US-08-612-973-9
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US-08-927-597-9
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361 CAGCTGTTCACCTTCTCACCTCGCCGCCATCAAACAGTACAGGACTGCAATCTGCTCAATC 420
361 CAGCIGITCACCTICICACCTCGCCGCATCAAACAGTACAGGACTGCAACTGCTCAATC 420
                                                                                                                                                                               us-08-927-597-11
; Sequence 11, Application US/08927597
; Patent No. 62452703
; GRUERAL INPORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXOW & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ALLINGTON
STATE: VIRGITAL
                                                                                                                                                 421 TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCCTA
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COMPUTER: IN PC COMPATIBLE

COMPUTER: IN PC COMPATIBLE

COMPUTER: PATENTIN PC COMPATIBLE

CURRENT APPLICATION DATE:

PRIJING DATE:

TILING DATE:

TILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKEY NUMBER: 1487-10

TELEPHONEY (ACRT NUMBER: 1487-10

TELEPHONEY (ACRT NUMBER: 1487-10

TELEPHONEY: (703) 816-4100

INFORMATION POR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 480 base pairs

TYPE: nucleic acid

TELEGTH: ASIDER SECONDER

TELEGTH: ASIDER

TYPE: THE THE THE THE THE TELEGTH: ASIDER

TYPE: THE THE THE THE THE THE THE TELEGTH: ASIDER

TYPE: THE THE THE THE THE THE THE THE THE TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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FEATURE:
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HYPOTHETICAL:
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LOCATION:
FEATURE:
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; LOCATION:
US-08-927-597-11
                                                                   셤
                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCIGCTITCIGITCCGCIAIGIACGIGGGGGATCTCTGCGGGATCTGTITTCCTTGTITCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AGGAACGCCAGCGTCCCCACAACGACATACGACGCCACGTCGATTTGCTCGTTGGGGGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGCTTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGGATCTGTTTTCCTTGTTTCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT
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                                 APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS POR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                       CUNTRY: AKLINGION

CTATE: AKLINGION

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: INPORMATION:

NAME: BPLICATION NUMBER: 32,205

REGISTRATION NUMBER: 32,205

REGISTRATIO
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   DE MARTYNOFF, GUY
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Matches 476; Conservative
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                                                                                                                                                                                                                                                                                    CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAMB/KEY:
LOCATION:
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US-08-612-973-11
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Gaps

181

301

361

925

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Sequence 14, Application US/08470426B

Patent No. 5856458
GENERAL INFORMATION:
APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Tetauo
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B.
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B.
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B.
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B.
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B.
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-B.
STREET: ADDRESSEE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
CITTY: Washington
                                                                                                                                                                                                                                                                                                                                                                             GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCCACGCTCGCGGCAAA
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                                                                                                                                      506 IGCCCGGTTGCTCTTTCTCTTTCTTCTTCTTGGCTTTGCTGTCTGTTTGACCATCCCAG
                                                                                                                                                                                             2 TGCCCGGTTGCTCTTTCTCTATCTTTGGCCCTGCTGTCCTGTCTGACCATACCAG
                                                                                                                                                                                                                                                                            GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
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                                                                                                                                                                                                                                                                                                                                                        GCGTTCGGGAGGCCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCCA
                                                                            Gaps
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                                   Length 1539;
                                                                            Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                              56;
                                     Score 433.4; DB 2;
Pred. No. 1.2e-113;
                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/470,426B FILING DATE: 06-JUN-1995 CLASSIFICATION: 536
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APPLICATION NUMBER: JP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Weilacher, Robert G. REGISTRATION NUMBER: 20,531
                                     89.7%;
94.5%;
                                                         Best Local Similarity 94.5
Matches 449; Conservative
                                     Query Match
Best Local Similarity
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US-08-470-426B-14
  US-08-470-426B-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Teteuo
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           300
TGGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCC 240
                                                                                                                                                                                                                                                                                                 GCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTTCCTTGTTTTCC 360
                                                                                                                                                                                                                                                                                                                   CAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATC 420
                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCTGTTCACCTTCACCTCGCCGCCATCAAACAGTACAGGACTGCAACTGCTCAATC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                             479
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                                                                                                                                                                                                                                             AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGATTTGCTCGTTGGGCT
                                                           AGGAACGCCAGGGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: RADAPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM COMPUTER: US/08/470,426B
FILING DATE: U6-JUN-1995
CLASSIFICATION NUMBER: UP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wellacher, Robert G.
REGIGTRATION NUMBER: 06/59-47083.1
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION OF SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1539 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young, ADDRESSE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08470426B Patent No. 5856458 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE:
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Score 430.2; DB 3;
Pred. No. 1.7e-112;
0; Mismatches 28;
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94.1%; Pred. No. 1.7e-112;
ive 0; Mismatches 28;
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, Sequence 6, Application US/09014416
, Patent No. 6153421
, GENERAL INFORMATION:
                   Query Match
Best Local Similarity 94.1%;
Matches 447; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) TYPE: DNA
) ORGANISM: Hepatitis C virus
US-09-014-416-6
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Patent No. 6153421
GENERAL INPORMATION:
APPLICANT: Wanagi, Masayuki
APPLICANT: Bukh, Jons
APPLICANT: Bukh, Jons
APPLICANT: Bukh, Jusanne U.
APPLICANT: Bukh, Jusanne U.
APPLICANT: Bukh, Jusanne U.
APPLICANT: Bukh, Jusanne H.
TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 20264276
CURRENT APPLICATION NUMBER: US/09/014,416
CURRENT APPLICATION NUMBER: US 60/053,062
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 9595
                                                                                                                                                                                                                                                                                                                                                                                                                                          1130 CTGCTTTCTCTCCCCCTATGTACGTGGGGGATCTCTCTGCGGATCTGTTTTCCTCGTCTCCC 1189
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                                                                                                                                                                                                                       Length 1863;
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                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                   Score 433.4; DB 2;
Pred. No. 1.3e-113;
0; Mismatches 26;
            TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
TELEPAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1863 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                             TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
US-08-470-426B-14
                                                                                                                                                                                                                 89.7%;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-4
                                                                                                                                                                                                                Query Match
Best Local Similarity 94.5
Matches 449; Conservative
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APPLICANT: Yanagi, Masayuki
APPLICANT: Bukh, Jens
TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE REPERENCE: 20264276
CURRENT APPLICATION NUMBER: US 60/053,062
EARLIER PILING DATE: 1998-01-27
BARLIER PILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PAFENTIN Ver. 2.1
SEQ ID NO 6
ILENGTH: 9599
                                                                                                                                                                                                                                                                                                                                                                                                           1027 GTGTTCAGGAGGGTAACAGCTCCCGTTGGTTGGGTAGCGCTCACTCCCACGCCGCGGGCCA 1086
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Length 9595;
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Sequence 20, Application US/08483695

Patent No. 5866139
GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Parabow, Garrett &
ADDRESSER: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848 TGCCCGGTTGCTCTTTCTCTTTCTCTCTTGCTCTGCTGTCTTGTTTGACCACCCCAG 907
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,695
                                                                                                                                                                             Score 425.4; DB 4;
Pred. No. 4e-111;
0; Mismatches 31;
                                                                                                Fig.
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SEQUENCE DESCRIPTION: SEQ ID NO: 96
US-08-150-204E-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1300 I Street, N.W. CITY: Washington
              STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                             Query Match 88.1%;
Best Local Similarity 93.5%;
Matches 444; Conservative (
TYPE: nucleic acid
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US-08-483-695-30
                                                                               FEATURE
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                                                                                              GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
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LEB, Yong Beom
PARK, Young Woo
LIM, Kook Jinn
CHOI, Deog Young
SO, Hong Seob
KIM, Chun Hyung
KIM, Sung Taek
YANG, Jae Young
TITLE OF INVENTION: HEBATITIS C DIAGNOSTICS AND VACCINES
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Desjeon
STATE: Desjeon
COUNTRY: Republic of Korea
COUNTRY: Republic of Korea
ZIP: 305-340
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM FC/Pentium
OPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word
CURRENT APPLICATION NUMBER: US/08/150,204E
FILING DATE: 20-Apr-1994
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: YANG, Jae Young
STREET: 386-1, Doryong-dong, Yuseong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Shahan Islam, B9q.
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER: 2695/FLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 91-9510
FILING DATE: 10-UNN-1991
APPLICATION NUMBER: KF 91-13601
FILING DATE: 6-AUG-1991
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 96, Application US/08150204B
Patent No. 6538126
GENERAL INFORMATION:
APPLICANT: CHO, Joong Myung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 940-8564
TELEFAX: (212) 940-8776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 9472 base pairs
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US-08-150-204E-96
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Patent No. 5879904
GENERAL INPORMATION:
APPLICANT: Exembort, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCA 276
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                                                                                                                                                                                                                                                                                                                                                                      Score 425; DB 2; Length 501;
Pred. No. 2.1e-111;
0; Mismatches 25; Indels
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         PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-WAR-1993
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATTORNEY-AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: Other
DESCRIPTION: cDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.6%;
Matches 440; Conservative
                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 30 SEQUENCE CHARACTERISTICS: IENGTH: 501 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         linear
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                    US-08-483-695-30
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US-07-965-285-30
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88.0%; Score 425; DB 2; Length 501;
Best Local Similarity 94.6%; Pred. No. 2.1e-111;
Matches 440; Conservative 0; Mismatches 25; Indels
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                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: BACENITH Release #1.0, Version #1.25
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR-1993
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REGISTRATION INFORMATION:
TELEPHONE: 202-408-4000
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Gal
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: RIORY disk
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INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
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APPLICANT: Brechot, Christian
APPLICANT: Kremedorf, Dina
APPLICANT: Kremedorf, Dina
APPLICANT: Forchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           397 AGCTGTTCACCTTCTCGCCTCGCCGGCATGAGACAGTGCAGGACTGCAACTGCTCAATCT 456
                                                                                  AGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT 421
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ADDRESSEE: Dunner
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CURRENT APPLICATION DATA:
PILING DATE:
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05286-0001-00000
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APPLICATION NUMBER: 07/965,285
PILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
RESTRATION NUMBER: 05.86-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 30, Application US/09201912; Patent No. 6210962
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SEQUENCE CHARACTERISTICS:
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EDNESS: single
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Best Local Similarity
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TOPOLOGY: lin
MOLECULE TYPE:
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                                                                         Sequence 30, Application US/08487231
Patent No. 5919454
GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Forchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 GCGTTCGGGAGGACAACAGCTCCCGTTGCTTGCGTAGCGCTCACTCCCACGCTCGCGGCCA 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Parabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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Pred. No. 2.1e-111;
O; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05286-0001-02000
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APPLICATION NUMBER: US/08/487,231
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/965,285
FILING DATE: 18-MAR-1993
CLASSIFICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: cDNA to genomic RNA
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARATTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.0%;
94.6%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 440; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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RESULT 12
US-08-487-231-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-487-231-30
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                                                                                                                                                                                                                                                                 Gaps
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Sequence 1. Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
APPLICANT: BOSNAN, FONS
APPLICANT: BUYSE, NASIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: POTFIENS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSES: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                     Query Match 88.0%; Score 424.8; DB 3; Length 642; Best Local Similarity 93.3%; Pred. No. 2.6e-111; Matches 444; Conservative 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PENTIN RElease #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: NIXON & VANDERHYE |
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
21P: 22201-4714
COMPUTER READABLE FORM:
                                                                                                                                  mat_peptide
1..636
                                                                                       1..639
                      ANTI-SENSE: NO FEATURE:
    HYPOTHETICAL:
                                                              US-08-927-597-3
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                                                                217 GOSTICGGGAGACAACAGCICCCGIIGCIGGGIAGCGCTCACTCCCACGCTCGCGGCCA 276
                                                                                                                                                                                                                                                                                                        GGAACGCCAGCGTCCCCACAACAACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOSTICGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA 241
                                                                                                                                                                                                                                                                                                                                                                                                 CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTTGTTTTCCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTGTTCACCTTCTCACCTCGCCGCATCAAACAGTACAGGACTGCAACTGCTAATCT 421
TGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCCTGTTTGACCATCCCAG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DO WARTYNOFF, GU
APPLICANT: DE WARTYNOFF, GU
APPLICANT: BUYSE, MARTYNOFF, GU
APPLICANT: BUYSE, MARTYNOFF, GU
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPRUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
SOFTWARE: Petentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERNE, THOOMARTION:
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 Arccceccarrrarcacercaccarecrreceararearea 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYB P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
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US-08-612-973-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGCCCGGTTGCTCTTTCTTTCCTCTTGGCCCCTGCTGTCCTGT
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHAX: (703) 816-4100
TELECHAX: (703) 816-4100
TELEPRAX: (703) 816-4100
TELEPRAX: (703) 816-4100
TELEPRAX: (703) 816-4100
TELEPRAY: (703) 816-4100
TELEPRAX: 11mear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KRY: CDS
LOCATION: 1..639
FEATURE:
NAME/KRY: MAT_PEPLIGE
NAME/KRY: MAT_PEPLIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.0
Best Local Similarity 93.3
Matches 444; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-927-597-3
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Search completed: June 16, 2004, 13:30:23 Job time : 35.8162 secs

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Query
                                                                                                                                           Result
                                                                                                                                                                                              June 16, 2004, 08:32:08; Search time 1464.4 Seconds (without alignments) 14206.949 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                      480
1 AIGICCGGIFGCICTTICTC.....TGATGATGAACTGGTAAIAG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6940544
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY NUC Gapoxt 1.0
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1: gb_ba:*
2: gb_htg:*
3: gb_ntg:*
4: gb_on:*
5: gb_ov:*
7: gb_ph:*
10: gb_ov:*
11: gb_pt:*
10: gb_ro:*
11: gb_ro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                 US-09-899-303A-11
                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                      Run on:
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Watch	Length	DB	ID	Description
	480	100.0	1 4	و	A48673	A48673 Semience 11
	480	100.0		9	AR157328	
	480	100.0		9	AX452760	
	480	100.0		ωv	AX685012 AY794854	AX685012 Sequence av794854 Sequence
	2 7	98.8		o	A48671	A48671 Sequence 9
	2.5	98.8		9	AR157327	AR157327 Sequence
	4.2	8.8		y v	AX452758	AX452758 Sequence
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                                                                                                   100.0%; Score 480; DB 6; L
llarity 100.0%; Pred. No. 7.2e-113;
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
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100.0%; Pred. No. 7.2e-113;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Plaviviridae;
Hepacivirus.
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                                                tch 100.0%; Score 480; DB 6; Length 4 al Similarity 100.0%; Pred. No. 7.2e-113; 480; Conservative 0; Mismatches 0; Indels
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Patent: WO 03051912-A 11 26-JUN-2003;
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/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"
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Patent: WO 02055548-A 11 18-JUL-2002;
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/protein id="CAA03131.1"
/db_xref="fG1:2302385"
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Maertens, G., Bosman, F., De, M.G. and
PURIFIED HEPATITIS C VIRUS ENVELOPE
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INNOGENETICS NV (BE)
Other publication CA 2172273 960215
Other publication AU 3382495 960304
Location/Qualifiers
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/mol_type="unassigned DNJ
/db_xref="taxon:32644"
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Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
Purified hepatitis C virus envelope proteins for diagnostic and
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98.8%; Score 474.2; DB 6; 99.4%; Pred. No. 2.2e-111; ive 0; Mismatches 3;
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Patent: US 6245503-A 9 12-JUN-2001;
Location/Qualifiers
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/mol_type="unassigned DNA"
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AR157327
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Qy 181 TGCGTTCGGGAGGCAACTCCTCCCGTTGCTGGCGCTCACGCTCCCACGCTCGCCGCCC 240	Db 241 AGGAACGCCCCACACACACACACACACACACCCACGCCACGTCGTTTGTTT	Db 301 GCTGCTTCTGTTGTAGTGGGGGATCTCTGCGGTTTTTCCTTGTTTCC 360 361 CAGCTGTTCACCTTCTCACCTGGGGATCTAAAGAGTACAGGACTGCTAAATC 420	DD 361 CAGCTGTTCACCTTCTCCCCGGCATCAACAGTACAGGACTGCTACAATC 420 ON 421 TATCCCGGCTATCAACTACCACCACACAACAACAACAACAACAACAATCCAAT	421 TATCCCGGCCATGTATCAGGTCACCGCATGGCTTCGGGATATGATGATGATGACTCCTA		_	AUTHORS Maertens, G., Bosman, F. and Buyse, M.A. TITLE Purified Hepatitis C Virus envelope proteins for diagnostic and therapeutic use therapeutic use and JOURNAL Patent: WO 02055548-A 9 18-JUL-2002; INNOGRNETICS N.V. (BB)	FEATURES Location/Qualifiers source 1483	/organism="Hepatitis C virus" /mol_type="unassigned DNA" /db_xref="taxon:11103" CDS 1. *Annamed brotein product"	/ Codon start=1 / protein_id="CaD86522.1" / db_xref="RightRemal: CAD86522." / db_xref="dispenses: CAD86522." / db_xref="lightRemal: CAD86522."	Query Match 98.8%; Score 474.2; DB 6; Length 483; Best Local Similarity 99.4%; Pred. No. 2.2e-111; Matches 476; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	1 AIGTCCGGTIGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCTGTCTG	61 GCTTCCGCTTATGAMSTGCGCAACGTSTCCGGGGTTATCATGTCACGAACGACTCCCGGGTTATGAAGAGCGCGAACGTGCCGGGGTTACCATGTCACGAACGA	Oy 121 AATTCAAGATATGTATGAGGCAGGGACATGATGATGAGCCCCGGGGTGCCT 180
Db 121 AACTCAAGCATAGTGTATGAGGCAGCGGACATGATGCACCCCCGGGTGCGTGC	Qy 241 AGGAACGCCAGGGTCCCCACAACGACAATACGACGACGACGTCGATTTGCTCGTTGGGGCT 300 Db 241 AGGAACGCCAGCGTCCCCCACAACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT 300	OY 301 GCTGCTTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCCTTGTTTTCC 360	Qy 361 CAGCTGTTCACCTTCTCACCTGGCGGCATCAAACAGTACAGGACTGCAACTGCTCAATC 420 Db 361 CAGCTGTTCTCACCTGGCGGCAACAACAGTACAGGAACTGCTAATC 420	421 TATCCCGGCCAFGTATCAGGTCACCGCAFGGCTTGGGATATGATGAACTGGTAATA 4 [RESULT 8 AX452758 AX452758 AX452758 AX452758 AX452758 AX652758 ACCESSION AX452758 ACCESSION AX452758 AX652758 AX652758 AX652758 AX652758 AX652758 AX652758	NORINGES Hepatitis C virus ORGANISM Hepatitis C virus Viruses; 88RNA positive-strand viruses, no DNA stage, Flaviviridae;	Hepacivirus. REFERENCE I AUTHORS Maertens, G., Bosman, F., de Martynoff, G. and Buyse, M.A. TITLE Recombinant vectors for producing how envelope proteins JOURNAL Patent: BP 1211315-A 9 05-JUN-2002;		source 1483 /organism="Hepatitis C virus" /mol_type="unassigned DNA" /db_xref="taxon:11103" CDS 1480	at_peptide	ORIGIN Query Match 98.8%; Score 474.2; DB 6; Length 483; Best Local Similarity 99.4%; Pred. No. 2.2e-111; Matches 476; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	IGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCTGTCTG	Qy 61 GCTTCCGCTTATGAAGTGCGCAACGTCTCCCGGGGTGTACCATGTCACGAACGA	Oy 121 AACTCAAGCATAGTGTATGAGGGGGGGGGCATGATCATGCACACCCCGGGTGCGTGC

	AX794852 AX794852 ION AX794852 NAS94852 NAS94852 NAS94852.1 GI:37515741 BS Hepatitis C virus Viruses, seRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepaciviris C virus Viruses, seRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacitis C virus NISM Hepatitis C virus envelope proteins for diagnostic and therapeutic use Location/Qualifiers INNOGENETICS N.V. (BE) Location/Qualifiers INNOGENETICS N.V. (BE) Location/Qualifiers Vorganism="Hepatitis C virus" // dD_xref="unnamed protein product" // dD_xref="unnamed protein product" // dD_xref="GI:37515742" // dD_xref="GI:37515742" // dD_xref="GI:37515742" // dD_xref="GI:37515742" // froduct="unnamed" // dD_xref="GI:37515742" // product="unnamed" // dD_xref="Unnamed" // dD_xref="Unn	Query Match 98.8%; Score 474.2; DB 6; Length 483; Best Local Similarity 99.4%; Pred. No. 2.2e-111; 0; Gaps 0; Matches 476; Conservative 0; Mismatches 3; Indels 0; Gaps 0; 1 ATGTCCGGTTGCTCTTTCTCTTTTCTCTTTGGCCTGCTGTCTGTCTTGACCATACCA 60 61 1 ATGCCGGTTGCTTTCTCTTATCTTTTCTCTTTGGCCTGTCTGT
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AQGLIRVCKLVRKVAGGHYVQMALMKLAALTGTYVYDHLFPLRDMAHAGLRDLAVVB
PVIFSDMETKVITWGADTAACVNIISGLPVSARRGKEILLGFADSHEGRGWRLLAPIT
                                                                                                                                       GCIGCTITCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCC 360
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241 AGGAACGCCACCACCACCACCACCACATACCACCCACGTCGATTTGCTCGTTGGGGCT 300
241 AGGAACGCCACCACCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT 300
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421 TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGATGATGACTCGTCCTA 479
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/noTe="isolated from a patient with liver cirrhosis and
hepatocellular carcinoma (HCC-5)"
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2 (bases 1 to 9379)
Nagayama,K., Kurosaki,M., Bnomoto,N., Miyasaka,Y., Izumi,N. and
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Submitted (23-NOV-1999) Second Department of Internal Medicine,
Tokyo Medical and Dental University, 1-5-45 Yushima Bunkyo-ku,
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Hepatitis C virus strain MD25 complete genome.
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/codon_start=1
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1880 bp RNA linear VRL 16-MAY-1998 Hepatitis C virus gene for structural protein, partial cds, 1608832
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Hepatitis C virus
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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GVNYATGNLECCSFGI FLLALLSCI.TI PASSY YEVRNYSGI YHTTNDCGNSSI YYKAAD
MIMHTPGCVPCVREDNSSRCWYALT PTLAARNASVPTTTI RHVDLLUGAAAPCSAMY
VGDLCGSVELVSQLFTFS PRHETVOOCNCSI YPGHLSGFRWADDMANNSPTTALVV
SQLLAI PQAVVDMYAGAHWOVLAGLAY YSWCRWAKVLI VALLFASOVDGETTYSGCAA
SHTTSTLASLF SPGASQRI QLVNTNGSWHINRTALNCNDSLHTGFLAALFYTHRFNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                   Okamoto, H., Okada, S., Sugiyama, Y., Kurai, K., Iizuka, H., Machida, A., Miyakawa, Y. and Mayumi, M.
Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a human carrier: comparison with reported isolates for conserved and divergent regions
J. Gen. Virol. 72 (Pt 11), 2697-2704 (1991)
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Analysis of the core and RI envelope region sequences of variant of hepatitis C virus obtained in Indonesia
Arch. Virol. 136 (1-2), 53-62 (1994)
                                                                                                                                                                                                                                                                                                                               genome
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Okamoto, H., Okada, S., Sugiyama, Y., Yotsumoto, S., T.
Yoshizawa, H., Tsuda, F., Miyakawa, Y. and Mayumi, M.
He S'-terminal sequence of the hepatitis C virus of Jpn. J. Exp. Med. 60 (3), 167-177 (1990)
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/note="82 bp upstream of Styl site"
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/note="putative"
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AUTHORS
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unclassified.

I (bases 1 to 2540)

S Okamoro, H. and Nakamura, T.
DETECTION SYSTEM FOR NON-B HERATITIS VIRUS RELATING ANTIGEN
AND ANTIBODY, POLYNUCLEOTIDE AND POLYPEPTIDE
AND ANTIBODY, POLYNUCLEOTIDE AND POLYPEPTIDE
AND ANTIBODY, POLYNUCLEOTIDE AND POLYPEPTIDE
NAKAMURA TETSUO
CS Hepatitis nona nonB virus
PN 79 193901884-A/2
PN 19 193901884-A/2
PN 10-APR-1993
PP 10-APR-1993
PP 10-APR-1991 JP 1991196175
PR 12-JUN-1990 JP 90P 304405 PI
CXAMOTO HIROAKI, NAKAMURA TETSUO
PC C12N15/51, C07K13/00, C12N15/06, C12P21/08, G01N33/576,
PC G10N133/577;
CC topology: Linear;
CC topology: Linear;
CC anti-sense: No;
FR Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 1027 GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGGCCA 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1087 GGAATGCCAGTCCCCACTACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGGGG 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1207 AGCTGTTCACCTTCTCGCCTCGCCGGCATGAGACAGTGCAGGACTGCAACTGCTCAATCT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E04805 25-terminal region of gRNA of Hepatitis nonA nonB virus.
                                                                                                                                                                                                                                                           1267 ATCCCGGCCATTTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCA 1322
                                                                                                                                                                                                                 847 TGCCCGGTTGCTCTTTCTCTTCTTCTTTGCTTTGCTGTTTTGACCATCCCAG
                                                                                                                                                                                                                                                                                         TGTCCGGTTGCTCTTTCTCTTTCCTCTTGGCCCTGCTGTCCTGTCTGACCATACCAG
                                                                                                                                                                                                                                                                                                                                                                                             GCGTTCGGGGAACTCCTCCGTTGCTGGGGGGGCGCTCACTCCCACGCGCGCCA
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                                                                                                                                                          Gaps
                                                                                                                  90.2%; Score 432.8; DB 6; Length 2540;
llarity 94.3%; Pred. No. 1e-100;
Conservative 0; Mismatches 27; Indels 0;

    .2540
    /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

     Location/Qualifiers
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E04805.1 GI:2173001
JP 1993091884-A/2.
unidentified
unidentified
                                                                                                                                     Similarity
                                                                                                                                                   Matches 449;
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E04805
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TITLE
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unclassified.

1 (Dases I to 2540)

1 (Dases I to 2540)

1 (Dases I to OldOutoreDay I to 2540)

VIRUS UGING OLIGOUTORE PRIMER AND OLIGONUCLEOTIDE PRIMER ALL P 1993023200-A 2 02-FBB-1993;

VIRUS UGING OLIGOUTORE PRIMER AND OLIGONUCLEOTIDE PRIMER NAXAMURA TERSUO

NAXAMURA TERSUO

PN 97 1993023200-A/2

PN 79 1993023200-A/2

PN 79 1993032300-A/2

PR 26-APR-1991 JP 1991191376

PR 26-APR-1990 JP 90P 153402

PR 26-APR-1990 JP 90P 153402

PR 0XAMOTO HIROAXI, NAXAMURA TERSUO

PC C1201/68,C12015/51,C1201/70;

CC topology: Linear;

CC topology: Linear;

CC *Source: strain=HC-J4;

FH Key Location (Qualifiers)

FT misc_feature 1. 2540

FT // Note = 'a part of type non-A non-B hepatitis

FT virus'.
GCPERMASCRPIDWFAQGWGPITYTEPDSPDQRPYCWHYAPRPCGIVPASQVCGPVYC
FTPSP"
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                                                                                                                                                                                                     GCGTTCGGGGAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                          GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
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0
                                                                 Score 432.8; DB 14; Length 1880;
Pred. No. 1e-100;
0; Mismatches 27; Indels 0;
                                                                 Query Match
Best Local Similarity 94.3%;
Matches 449; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E04260.1 GI:2172463
JP 1993023200-A/2.
unidentified
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E04260
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/organism='Hepatitis non-A
                               Location/Qualifiers
topology: Linear;
hypothetical: No;
                      anti-sense: No;
                                                                                             mat_peptide
                                                                                                                                        mat_peptide
                                                     Bource
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                                                                                                                                                                         5
         TR 1. .341
342. .2540
/note=: protein coded by Hepatitis nonB virus gene'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
unidentified
unidentified
unidentified
unidentified
unclassified.
1 (bases 1 to 2540)
Okamoto, H. and Nakamura, T.
Okamoto, H. and Nakamura, T.
PATENTENENTIES VRUE IN HIGH SENSITIVITY
PATENTY VRUE IN HIGH SENSITIVITY
PATENTY PRESSUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1991 JP 1991247120
OKAMOTO HIROAKI, NAKAMURA TETSUO
CIZNI5/51,CIZN1/21,CIZP21/02,CIZQ1/70,G01N33/53,G01N33/569,
                                                                                                                                                                                    847 IGCCCGGTIGCTCTTTCTCTATCTTCCTCTTGCTTTGCTGTCTGTTTGACCATCCCCGG
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                                                                                                                                                    Gaps
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                                                                                                                            90.2%; Score 432.8; DB 6; Length 2540; llarity 94.3%; Pred. No. 1e-100; Conservative 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E07391 2540 bp RNA linear P CDNA encoding chimpanzee hepatitis non-A non-B virus.
                                                              1. .2540
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis non-A non-B virus
JP 1994125777-A/4
10-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strandedness: Single
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          S'UTR
                   SOS
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                                                                                                                             Query Match
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E07391
                                                                                                                                                Matches
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AUTHORS
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                                                                                              1491. .2540
/note='Structural protein of chimpanzee
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                                                                                                                                                                                                                                                                                                       Length 2540;
                                                                                                                                                                                                                                                                                                                                          Indels
1. .341
342. .1490
/note='non-structural pi
hepatitis non-A
non-B virus'
                                                                                                                                                                                                                                                                                                     Query Match 90.2%; Score 432.8; DB 6; Best Local Similarity 94.3%; Pred. No. 1e-100; Matches 449; Conservative 0; Mismatches 27;
                                                                                                                                                                  Location/Qualifiers
1. .2540
/organism="unidentified"
                                                                                                                                 hepatitis non-A
non-B virus'
                                                                                                                                                                                                                              /mol_type="genomic RNA"
/db_xref="taxon:32644"
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Job time : 1465.4 secs
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June 16, 2004, 07:39:53 ; Search time 180.6 Seconds (without alignments) 11290.892 Million cell updates/sec
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1 AIGTCCGGTTGCTCTTTCTC.....TGATGATGAACTGGTAATAG 480
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version 5.1.6
- 2004 Compugen Ltd.
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                                                                    - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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   GenCore
Copyright (c) 1993
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seq length: 200000000
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                                                                                                                                                                                                                                              IDENTITY NUC
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Perfect score:
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Maximum DB 9
                                                                      OM nucleic
                                                                                                                                                                                                            Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID Description	AAT12708 HCV R1 CC	Aa148917		AAT12707 HCV B1 CO		ADD55517 Hepatitis		Aba03491	Aaq43889		Aaq15363	AAQ29628 Hepatitis	•	AAF23492 Infection	AAC86939 Aac86939 Nucleotid	AAX24833 Aax24833 Infection	AAQ35081 Aaq35081 HCV envel	ABA03492 Aba03492 Cuticle p	AAT12706 AAT12706 HCV El CO	AAL48915 Hepatitis	ADD55515 Add55515 Hepatitis	
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Length	480	480	480	483	483	483	1880	2187	2540	2540	1863	2540	9595	9595	9595	9599	577	2187	633	633	633	1
& Query Match	100.0	100.0	100.0	98.8	98.8	98.8	90.2	90.2	90.2	90.2	89.8	89.5	89.2	89.2	89.2	89.2	88.8	88.8	88.8	88.8	88.8	
Score	480	480	480	474.2	474.2	474.2	432.8	432.8	432.8	432.8	431.2	429.6	428	428	428	428	426.4	426.4	426.2	426.2	426.2	
Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	ć

Aaq11076 Fragment Aaz07647 HCV J1 B Aav60672 Fragment Aa155222 Plasmid n					Add55634 Heparitis Aaq27159 NAWB hepa Aaq35086 HCV envel Aaq79758 Heparitis
AAQ11076 AAZ07647 AAV60672 AAISC222	AAX 00401 AAX 00401	AAX26728 AAQ79772 AAX26739	AAV60668 AAQ64069 AAT30387	AAT12704 AAT12704 AAL48913	ADD55634 AAQ27159 AAQ35086 AAQ79758
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423 423 423 423	444	4 4 4	422.8 422.8 422.8	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	422.2 421.6 421.2 421.2
24 25 26	3000	1000	3 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0 6 4 4 0 0 0 1	4 4 4 4 6 6 4 6

ALIGNMENTS

HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera; Buyse M; De Martynoff G, BP. 95WO-BP003031. 94EP-00870132. AAT12708 standard; DNA; 480 23-SEP-1996 (first entry) HCV El construct HCCI13A. (INNO-) INNOGENETICS NV Bosman P, WPI; 1996-129401/13. Hepatitis C virus. 29-JUL-1994; WO9604385-A2. 31-JUL-1995; 15-PBB-1996. Maertens G, AAT12708; RESULT 1

Claim 23; Fig 21; 146pp; English.

Purifying recombinant hepatitis C virus (HCV) B1 and B2 envelope proteins - in presence of dissulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.

and B2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant B1, B2, and B1/B2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage agent, after lysis of recombinant host cells. The constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serotyping assay for detecting one or more BJ AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV)

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serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1. E2 and B1/B2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
                                                                                                                                                                                                               1 ATGLCCGGTTGCTCTTTCTTCTTCTCTCTTGGCCCTGCTGTCCTGTCTGACCATACCA
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                                                                                                                                               Gaps
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                                                                                                                  100.0%; Score 480; DB 2; Length 480; 100.0%; Pred. No. 3e-130; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus clone HCCI13A E1 protein coding sequence
                                                                                              Sequence 480 BP; 85 A; 149 C; 123 G; 123 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2001; 2001US-0260669P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL48917 standard; DNA; 480
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                                                                                                                               al Similarity 100.
480; Conservative
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The present invention relates to new therapeutic vaccine compositions for inducing hepatitis C virus (HCW)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific Oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV B1 and/or B2 proteins are useful as vaccines or therapeutics, in HCV screening and confirmatory antibody tests, for raisang antibodies, in htb preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence
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                                                                           New therapeutic vaccine compositions comprising at least one purified recombinant hepatitis C virus (HCV) single or specific oligomeric recombinant envelope protein El or E2, useful for immunizing humans from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                               is a coding sequence described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACTCAAGCATAGTGTATGAGGCAGCCGACATCATGCACCACCCCCGGGTGCGCCC
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; Pred. No. 3e-130;
0; Mismatches 0;
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                                                                                                                                                       Example 2; Page 167-168; 243pp; English
 Buyse M;
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 Bosman F,
                               WPI; 2002-599657/64.
P-PSDB; AAO18664.
                                                                                                                        HCV infection.
 Maertens G,
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AAT12707 standard; DNA; 483
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                                                             23-SEP-1996
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                                                                                                                                                                                                                                                                                                                                            The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liver disease. The vaccine of the invention comprises an HCV El or E2 protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present DNA sequence encodes an HCV El protein.
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                                                                                                                                                                                                                                                                            New hepatitis C virus (HCV) vaccine composition, useful for reducing liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
          vaccine; liver disease; El protein; E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 480 BP; 85 A; 149 C; 123 G; 123 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 100.0%; Score 480; DB 9; sal Similarity 100.0%; Pred. No. 3e-130; 480; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 11; 271pp; English.
                                                                                                                                                                                                               Bosman F;
                                                                                                                      18-DEC-2002; 2002WO-EP014480
                                                                                                                                                 18-DEC-2001; 2001US-00020510
                                                                                                                                                           16-OCT-2002; 2002US-0418358P
                      liver fibrosis; ds; gene.
          C virus; HCV;
                                                                                                                                                                                      (INNO-) INNOGENETICS NV
                                                                                                                                                                                                              Depla E,
                                                                                                                                                                                                                                         WPI; 2003-541632/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                               Hepatitis C virus.
                                                                                                                                                                                                                                                    P-PSDB; ADD55520
                                                                      WO2003051912-A2.
                                                                                                                                                                                                               Maertens G,
                                                                                              26-JUN-2003
          depatitis
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and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide bond cleavage, or a reduction step with a disulphide constructs containing the purified HV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a serctyping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genetype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates containating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of disulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnostic assays of HCV.
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                                                                          HCV; B1; B2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Martynoff G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Fig 21; 146pp; English.
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HCV E1 construct HCCI12A
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                                                                                                                                                                                                                                Hepatitis C virus.
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liver fibrosis; ds; gene.
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                                                                                                                                                 1 ATGTCCGGTTGCTCTTTCTCTTCTTCTTGGCCCTGCTGTCCTGTCTGACCATACCA
                             Pred. No. 1.5e-128;
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                                                                    Mismatches
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99.4%; Pre-
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16-OCT-2002; 2002US-0418358P.
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                                                                    Conservative
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P-PSDB; ADD55518.
                         Best Local Similarity
Matches 476; Conser
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                                                                                                                                                                                                                                                                                                           TGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGCGCGCTCACTCCCACGCTCGCGGCC 240
                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCTGTTCACCTTCTCACCTCGCCGCATCAACAGTACAGGACTGCAACTGCTCAATC 420
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                                                                                                  AGGAACGCCAGGCTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT
                                                                                                                                                     GCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCTGTTCACCTTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus clone HCCI12A B1 protein coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buyse M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL48916 standard; DNA; 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-599657/64.
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AMA 8916 AMA 89

The invention comprises an Hepatitis C virus (HCV) vaccine for reducing New hepatitis C virus (HCV) vaccine composition, useful for reducing liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal

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(IMMO ) IMMUNO JAPAN INC
                                                                                       Recombinant
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                              Okamoto H,
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                                                                                                             Gape
liver disease. The vaccine of the invention comprises an HCV El or E protein as an antigen. The HCV vaccine is useful for reducing liver disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The present DNA sequence encodes an HCV El protein.
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amplification polymerase chain reaction; vaccine; antibody; ss.
                                                                                    Length 483;
                                                            Sequence 483 BP; 85 A; 152 C; 123 G; 123 T; 0 U; 0 Other;
                                                                                                            Indels
                                                                                   Query Match 98.8%; Score 474.2; DB 9; Best Local Similarity 99.4%; Pred. No. 1.5e-128; Matches 476; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NANB hepatitis virus strain HC-J4 genome.
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/label= HC-J4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccines and immunological pharmaceuticals and also to produce antibodies specific to NANBHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                        This sequence is the genome of the non-A, non-B hepatitis virus (NANBHV) strain HC-J4. This sequence was derived by amplification by polymerase chain reaction. The nuclectide sequences derived from this amplification can be used to detect NANBHV infection which could not be detected by conventional methods. The detection kits allow highly specific and sensitive detection at an early phase of infection. The polypeptide product of this coding sequence can be used for the manufacture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAACGCCAGCGTCCCCCAACAACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
                                                                                                                                    inant cDNA of NANBH virus strain HC-J5 and corresp. peptides - for diagnosis and in vaccines and immunological pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1027 GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACCCCCACGCTCGCGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 432.8; DB 2;
Pred. No. 3.2e-116;
0; Mismatches 27;
                                                                                                                                                                                                                     Disclosure; Page 11; 42pp; English.
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Matches 449; Conservative
Nakamura
                                                      WPI; 1992-160959/20.
P-PSDB; AAR24087.
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AAQ43889 standard; cDNA to mRNA; 2540 BP.
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P-PSDB; AAR38279.
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                                                                                                                                                                                                                                                                                                   10-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGGCCA 745
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                                                                                                                                                                                                                                                                                                                                   The present invention relates to cuticle protein 1 and 2 secreting hepatitis C virus. The present sequence is a coding sequence provided in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                     Cuticle protein 1 and 2 secreting hepatitis C virus (Japanese)
                                                                                                                                                                                                                                                                                                                                                                                                          ery Match 90.2%; Score 432.8; DB 2; Length 2187; st Local Similarity 94.3%; Pred. No. 3.4e-116; tches 449; Conservative 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2187 BP; 406 A; 669 C; 631 G; 481 T; 0 U; 0 Other;
                                                                     /partial
/note= "no stop codon"
                                                         "AAM47264"
                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Disclosure; Page 2-4; 7pp; Korean
                                                                                                                                                       96KR-00007404
                                                                                                                                                                             96KR-00007404
                                                                                                                                                                                                                           Choo SH, Lee IH, Ryoo WS;
                                              /*tag= a
/product=
                                                                                                                                                                                                                                                  WPI; 1998-492654/42.
P-PSDB; AAM47264.
                                                                                                                                                                                                    (GLDS ) LG CHEM LTD
                                                                                                       KR97065713-A
Unidentified
                                                                                                                                                     19-MAR-1996;
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of NANB hepatitis virus polynucleotide N-2540-2 which codes for a non-A, non-B (NANB) hepatitis virus gene HC-OM. The polypeptide it encodes may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by conventional methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen related to non-A and non-B hepatitis virus - comprises non-translation region comprising 340 - 341 mols. of nucleotides, non-translation region comprising 1885 - 2551 mols. of nucleotides including
                                                                                         Non-A, non-B; virus; polymerase chain reaction; detection; sensitive; specific; HCV; NANBH; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TGTCCGGTTGCTCTTTCTCTTTCTTTGGCCCTGCTGTCCTGTCTGACCATACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGGGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                        /*tag= b
/note= "from 5' terminal of NANBH virus RNA"
342. .2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2540 BP; 471 A; 775 C; 741 G; 553 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 432.8; DB 2;
Pred. No. 3.5e-116;
0; Mismatches 27;
                                              NANB hepatitis virus polymucleotide N-2540-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 19-20; 73pp; Japanese.
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90JP-00153401
90JP-00304405
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94.3%;
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 449; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region 1,149 and, etc.
                                                                                                                                                             Non-A.
non-B hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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GOGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCCACGCTCGCGGCCA 1086
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                                                                                                                                                                                                                   1207 AGCTGTTCACCTTCTCGCCCGCCATGAGACAGTGCAGGACTGCAACTGCTCAATCT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NANB hepatitis virus strain HC-J4 was isolated from a plasma sample of a chimpanzee challenged with NANB hepatitis for infectivity but which tested negative for HCV antibody by Ortho HCV AD BLISA test. NAN was isolated from the sample and reverse transcribed into CDNA. The 513 amino acids encoded by the CDS were determined but are not given in the specification (and hence are not included in A-Geneseq). A study of the deduced sequence suggested that the CDS encodes NANBH virus core proteins. Primers for detecting NANB hepatitis virus were designed based on the HC-44 sequence. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligo-nucleotide primers - derived from and used to detect and diagnose
                                                                                                                                                                                                                                                                                      1267 ATCCCGGCCATTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCA 1322
                                                    GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCTG
                                                                                      1087 GGAATGCCAGCGTCCCCACTACGACATACGACGCCACGTCGACTTGCTCGTTGGGGGGG
                                                                                                                                                                                              AGCTIGITICACCTTCTCACCTCGCCGCATCAAACAGTACAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                                                                       477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
422 ATCCCGCCCATGTATCAGGTCACCGCATGCCTTGCGATATGATGATGAACTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fragment of NANB hepatitis virus strain HC-J4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okamoto H, Ogikubo Y, Nakamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-A , non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                 AAQ15363 standard; DNA; 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91EP-00305270.
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325. .1863
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(IMMO ) IMMUNO JAPAN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
17-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1991.
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                  1027
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5'UTR
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                               CTGCTTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCCTTTTCCC 361
                                                                                      421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGGGGCGCTCACTCCCACGCTCGCGGCCA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAQ63752-53 represent fragments of the non-A, non B hepatitis virus (NANBHV) genome. These fragments were amplified using the primers given in AAQ63732-51. These primers were used in the detection of NANBH. The primers are based on the S'-terminal region and the core protein coding region. The method allows highly sensitive detection of NANBHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonuclectide primer pairs specific for non-A, non-B hepatitis virus used for high sensitivity detection of non-A non-B (NAMB) hepatitis
                                                                                                                                                     1207 AGCTGTTCACCTTCTCGCCTCGCCTGAGACAGTGCAGGACTGCAATCT
                                                                                  362 AGCIGITICACCTICACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IGTCCGGTTGCTCTTTCTCTTCCTCCTTGCCCCTGCTCCTGTCTGACCATACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                               Polymerase chain reaction; PCR; primer; amplify; detection; NANBHV; non-8, non-B hepatitis virus; 5'-terminal region; core protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.2%; Score 432.8; DB 2; Length 2540; 94.3%; Pred. No. 3.5e-116; live 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 2540 BP; 470 A; 775 C; 742 G; 553 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 24-25, 25pp; Japanese.
                                                                                                                                                                                                                                                                                 AAQ63753 standard; cDNA to mRNA; 2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91JP-00247120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91JP-00247120
                                                                                                                                                                                                                                                                                                                                                                                             NANBHV genomic fragment #2
                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 94.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP06125777-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                         30-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                          1267
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This sequence represents the 5' region of hepatitis C virus RNA. The original sample was obtained from human and chimpanzee plasma. RNA was isolated from several samples and homology comparted, and the respective sequence of about 1900 - 2500 mucleotides of the 5' terminus and 1100 nucleotides of the 5' region (given) contains a non-coding region of at least 340 nucleotides and a region coding for the structural protein followed by a region coding for protein (none actually detailed on the sequence given in the specification). When compared with the sequence of HCV disclosed in EP-38822 this sequence showed homology of 80.5%. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIGCTITICICCCCCTATGTACGTGGGGGATCTCTGCGGGATCTGTTTTCCTCGTCTCCCC 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGTTCGGGAGGACAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCA 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV; infectious clone; infection; diagnosis; therapy; vaccine; screening; assay; antiviral; virucide; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAATGCCAGCGTCCCCACTACGACAATACGACCACGTCGACTTGCTCGTTGGGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arccegecarttatcaggtcacecargecttgegarargargargacer 1322
                                                                                                                                                                                                                                                                                                                                      847 IGCCCGGTIGCTCTFTCTCTTCTTCCTCATGGCTTTTGCTCTTTTGACCATCTCCAG
                                                                                                                                                                                                                                                                                                                                                                             CHGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AGCTGTTCACCTTCTCACCTCGCCGCATCAACAGTACAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAA 477
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                             Length 2540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Infectious hepatitis C virus genotype 1b strain HC-J4 genome.
                                                                                                                                                                                                             Sequence 2540 BP; 472 A; 775 C; 741 G; 552 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                           Score 429.6; DB 2;
Pred. No. 3.1e-115;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
342. .9374
/*tag= a
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                                                                                                                                                                                                                                          Query Match 89.5%;
Best Local Similarity 93.9%;
Matches 447; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX24843 standard; DNA; 9595
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                                                                                                                                                                                                                                                                                                                                                                                                                           361
                                                                                                             241
                                                                                                                                                          Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening; PCR; primer; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide primers with nucleotide sequences corresp. to part. of the viral RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCCGGTTGCTCTTTCTCTTTCCTCTTGGCCCTGCTGTCTGTCTGACCATACCAG
                                                                                                                                                                                                                                                                                         GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         477
                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTCCTTTGTTTCCC
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAA
                                Score 431.2; DB 2; Length 1863;
Pred. No. 9.3e-116;
0; Mismatches 28; Indels 0;
Sequence 1863 BP; 333 A; 586 C; 547 G; 397 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 18; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus HC-J4 5' region.
                                 89.8%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91JP-00191376
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                                Query Match
Best Local Similarity 94.1
Matches 448; Conservative
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16-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to GB virus-B. The nucleic acid molecules of the invention are useful for indirectly studying the molecular properties of hepatitis C virus (HCV). HCV/GBV-B chimeras may be used sequence of the GB virus-B clone and the HCV/GBV-B chimeras may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New infectious nucleic acids of the GB virus-B clone, useful for indirectly studying the molecular properties of hepatitis C virus (HCV) and in developing vaccines and therapeutics for HCV.
                                                                                                     1267 ATCCCGGCCATGTATCAGGTCACCGCATGGGTTGGGGATATGATGATGAACTGGTCA 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGGATATGATGAACTGGTAA 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.2%; Score 428; DB 4; Length 9595; Best Local Similarity 93.7%; Pred. No. 1.5e-114; Matches 446; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the development of vaccines and therapeutics for HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GBV-B; hepatitis C virus; HCV; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                     Infectious Hepatitis C virus 1b genotype.
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                                                                                                                                                                                                                                             AAF23492 standard; DNA; 9595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence comprises the nucleic acid sequence of the genome of infectious hepatitis C virus (HCV) genotype 1b strain HC-J4 (ATCC 209596) that is capable of expressing this virus when transfected into cells. HC-J4 was obtained from acute phase plasma of a chimpanzee experimentally infected with serum containing HC-J4/91. The claimed infectious nucleic acid sequence can be used to produce chimeric genomes (see AAX14833) consisting of the open reading frames of infectious nucleic acid sequences of other genotypes (including genotypes 1.6) and subtypes (such sequences of other genotypes (including genotypes 1.6) and subtypes (sea bb, 2a, 2b, 2c, 3a, 4a-f, 5a and 6a) of HCV. The invention also calase to the introduction of mutations or deletions into infectious nucleic acid sequences can actenuated HCV virus suitable for vaccine development. Infectious nucleic acid sequences can also be used to produce attenuated virus via passage in vitro or in vivo of the viruses produced by transfection of a host cell with the infectious nucleic acid sequence. Vaccines comprising one or more polypeptides made from the infectious nucleic acid sequence ace used to infectious mumals, especially humans, against hepatitis C. The nucleic acid sequences can also be used to induce protective immunity against the virus. The nucleic acid sequences or their encoded proteases (e.g. NS) increase) can additionally be used to develop screening assays to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                            New isolated hepatitis C virus nucleic acids - used to develop products for the diagnosis, prevention and treatment of HCV infections and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GCGTTCGGGAGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGATTTGCTCGTTGGGGGCTG
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Best Local Similarity 93.7%; Pred. No. 1.5e-114;
Matches 446; Conservative 0; Mismatches 30;
                                                                                                                                                                                                             Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 14A-F; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dentify antiviral agents for HCV
                                                                                                                                                                                                             (anagi M, Bukh J, Emerson SU,
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                                            98WO-US014688
                                                                                           97US-0053062P
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                                                                                                                                                                                                                                                                                                                                                                                developing screening assays.
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                                          16-JUL-1998;
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                                                                                                                                                                                                                                                 Chimeric virus; bovine viral diarrhoea virus; BVDV; hepatitis C virus; HCV; vaccine; viral inhibitor; antiviral; ss.
                                                                                                                                    CTGCTTTCCTGTTCCGCTATGTACGTGGGGGATCTTGCGGATCTGTTTTCCCTTGTTTTCCC
                                                                                                          AGCTGTTCACCTTCTCACCTCGCCGGCATCAACAGTACAGGACTGCAACTGCTCAATCT
                                                                                                                                                                                                                 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a hepatitis C virus (HCV) clone genotype 1b.
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ilarity 93.7%; Pred. No. 1.5e-114;
Conservative 0; Mismatches 30;
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completed: June 16, 2004, 09:36:56 ne : 182.6 secs time

The specification describes a nucleic acid comprising a chimeric virus genome, specifically bovine viral diarrhoea virus (BVDV) genome in which the fun-) structural region has been replaced by the (non-) structural region of a hepatitis C virus (HVU) genome. The nucleic acids comprising the chimeric virus and the chimeric virus are useful for identifying cell lines capable of supporting the replication of these chimeric viruses, in creening for neutralizing antibodies to HCV of different genotypes, in the production of HCV-BVDV virious, for the development of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, in studying the molecular properties of HCV indirectly in virto, and in identifying inhibitors of viral enzyme activity which would be useful as antiviral agents. Formulations or compositions comprising the chimeric virions may be used to treat or prevent the signs and symptoms of HCV. The present sequence represents a HCV clone, which is used to construct chimeric concerns.

Sequence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 U; 0 Other;

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7

Scoring table:

Searched:

Minimum DB Maximum DB

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Database

Perfect score:

Sequence:

OM nucleic

Run on:

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 488)

2 (bu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Pu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,Z., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z. Homo sapiens cDNA BM clones

Unpublished (2000)

Contact: Zeguang Han

Contact: Zeguang Han

Contact: Zeguang Han

Contact: Zeguang Han

Tolis Go. Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919 (ex.45)

Fax: 86-21-50801919

Fax: 86-21-50801919

This clone is available at CHGC in Shanghai.
       CG213867 OGVCR53TV
CG313867 OGVCR53TV
CG31319 OGD18144TV
AN638521 AV638521
AV637507 AV637520
AV637507 AV637259
AV637259 AV637259
AV637259 AV637259
AV637259 AV637259
AV637259 AV637259
AV63726 AV637050
AV63726 AV637050
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AV63726 AV637050
AV637382 AV637050
AV637372 AV637050
AV637373 AV637050
AV637373 AV637050
AV637373 AV637359
AV637373 AV637359
AV637373 AV633739
CC63468 ABAŢ 1_D1
AV633658 AV633558
CC63468 ABAŢ 1_D1
AV633658 AV633558
CC734434 OGUPC24TV
BZ555011 pace1-60
AL101589 Drocophil
CC916826 C093009ba
CC734426 OGUPC24TV
BZ555011 pace1-60
AL101589 Drocophil
CC916826 C093009ba
CC73443 OGUPC24TV
BZ555011 pace1-60
AL101589 Drocophil
CC916826 C093009ba
CC73443 OGUPC24TV
BZ553034 OGALV23TC
CC734435 AV634529
CC734458 BX415186
BISS3034 OGALV23TC
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AV755731
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CG300832
CG213867
CC634840
CG373319
AL825643
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BX421743
AL565958
CD206870
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AV633658
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AV634724
AV637050
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AV632765
AV632811
AV392445
AV6341895
AV6341895
AV638125
AV633335
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  Homo sapiens (human)
Homo sapiens
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BZ645446 OGCBJ86TC
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    (without alignments)
11108.065 Million cell updates/sec
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AV758366 AV758366
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                                                                                                           1 AIGTCCGGTTGCTCTTTCTC.....TGATGATGAACTGGTAATAG
                                                                                                                                                                        55026578
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                     27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
                                         nucleic search, using sw model
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em_estpl:*
em_estpl:*
gb_est2:*
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65.8 54.6 43.2 41.6

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psHB036xB09f USDA-IFAFS:Expression of Phytophthora sojae genes
during infection and propagation_sHB Phytophthora sojae genes
sHB036B09 5, mRNA sequence.
                                                                                                                                                                                       368 TCACCTICTCACCTCGCCGGCATCAAACAGTACAGGACTGCCAACTGCTCAATCTATCCCG 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="mycelium"
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/clome lib="USDA-IPARS: Expression of Phytophthoxa sojae
genes during infection and propagation sHB"
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                                                                                                                                                                                                                                                                         428 GCCATGTATCAGGTC-ACCGCATGGCTTGGGATATGATGATGAACTGGT 475
                                                                                                                                                                                                                                                                                                 340 GCTGCATCACTACAGTATGGCATAGGCTATGATGATGATGGT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.0%; Score 43.2; DB 14; Length 534;
47.4%; Pred. No. 3.4;
tive 0; Mismatches 143; Indels 0;
                            Length 492;
                       Query Match 11.4%; Score 54.6; DB 9; Length 4 Best Local Similarity 65.7%; Pred. No. 0.0043; Matches 111; Conservative 0; Mismatches 54; Indels
                                                                                                         308 TCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1880 Pratt Dr., Blacksburg, VA 24061, USA

    .534
    /organism="Phytophthora sojae"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: BK reverse primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF846043.1 GI:38061697
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Tyler, B. Not Published
Unpublished (2003)
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PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 534)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Tyler B
Tyler lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phytophthora.
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Best Local Similarity
Matches 129; Conserv?
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AV758366 BM Homo sapiens cDNA clone BMFAKA03 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                     472 GIGGIGTCACACTCGCTCTGCTCACGTCTACGTGTGGACCTCTGCGACGGAGTGATG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                        CTIGITICCCAGCIGITCACCTTCACCTCGCCGCCATCAAACAGIACAGGACTGCAAC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 CTTGCAGTTCAGCTGATCA---TCTGGCCTCAGCACCATGAGTTTGTGCATGAATGCAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 492)
Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Qian,B., Liu,P., Qu,J., Gao,X., Cheng,Z., Xu,Z., Eng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Ru,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
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/clone=lib="RM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Zeguang Han
Contract: Zeguang Han
Contract of National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-508019122
Bmail: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Bone marrow"
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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                           Length 488;
                                                                                                                                                                                                                                                                                                                57; Indels
                                                                                                                                                                                                                                                                       13.7%; Score 65.8; DB 9;
llarity 67.0%; Pred. No. 6.3e-06;
Conservative 0; Mismatches 57;
                                           organism="Homo sapiens"
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Unpublished (2000)
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FEATURES
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COMMENT

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OGWJO7)3TV ZM 0.7_1.5 KB Zea mays genomic clone ZMMEMa0603M01, genomic survey sequence.
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CGVCR53TV ZM 0.7 1.5 KB Zea mays genomic clone ZMVBMa0506110, genomic survey sequence.
CG213867.1 GI:34113755
CG213867.1 GI:34113755
CG2 mays
Zea mays
Eas mays
Exe mays
                                                                                                                                                                                                               Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

( bases 1 to 741)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Praser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 CCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 CCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 CGTACCTGCGGTGCCGAGCCTCCACGAAGTGGTAGAAGCCCCTGCCGCTGCTGTTGGCGG
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methylation filtered genomic DNA library"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: whitelaw@tigr.org
                                                                                                                                        CG300832.1 GI:34215046
                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-5843
Fax: 301-838-0208
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Best Local Similarity
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CG213867/c
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GAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCAGGAACGCC 249
                                    320 CACTACGCCGCCCATCCTCGGCTCGAGCCGTGGTGGCTTCGACGTGGACAAGATTATC 379
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                                                                            250 AGCGICCCCACAACGACAATACGACGCCACGICGATTIGCTCGTTGGGGCTGCTGCTTTC 309
                                                                                                               380 AACTTCCTGACGACGACGGCGTCTCGCAGGTATACGTGATCGGCGGTGACGGCACCCCAC 439
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.,
Consortium for Maize Genomics
Other GSSs: OGCBJ657

Contact: Cathy Whitelaw
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/clone="zMmBMa0133P04"
/clone="zMmCMa013P04"
/note="vector: PBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Tel: 301-838-5843
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8.7%; Score 41.6; DE
Best Local Similarity 50.5%; Pred. No. 9.3;
Matches 101; Conservative 0; Mismatches
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/mol_type="genomic DNA"
/strain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                   BZ64546.1 GI:28107610
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Class: sheared ends.
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Seq primer: TF
Class: sheared ends
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           Tel: 301-838-5843
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1 (bases 1 to 995)
Whitelaw, C.A., Quackenbueb, J., Van Aken, S., Utterback, T., Click, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. L. (bases 1 to 744)
Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C. M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Other_GSSS: OGVCR53TH
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/clone="ZMMBMa0506110"
/clone=lib="ZM_0.71.5_KB"
/note="Vector: pBcSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                       Contact: Cathy Whitelaw
TIGR
TYT2 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
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9712 Medical Center Drive, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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Contact: Cathy Whitelaw
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CC634840.1 GI:32012237
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OG1B144TV ZM 0.7_1.5_XB Zea mays genomic clone ZMMBMa0723H15,
genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (basea 1 to 761)
Whitelaw.C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
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methylation filtered genomic DNA library"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                organism="Zea mays"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
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Other_GSSs: OG1BI44TH
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us-09-899-303a-11.rst

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/clone lib="Chamydowonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
                                                                                                                                                                                                                   linear BST 15-DBC-2000
Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Brika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu&kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Chlamydomonas reinhardtíi
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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1 (basea 1 to 399)

Asamizu, B., Miura, K., Kucho, K., Inoue, Y., Pukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii

DNA Res. 7 (5), 305-307 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 CATGGGCATCTACGGTCCCCGCACCGTGTTCTCCATTGCCCTGAAGGACGCCCCCGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 399
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                                                                    270 ACGACGC 276
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                                                                                                                                                                                         41 TGTCCTGTCTGACCATACCAGCTTCCGCTTATGAAGTGCGCAACGTGTCCCGGGTGTACC 100
                                                                                                                                                                                                                              303 ACAGCCCCGGGGGTGGTCCGCGTCCTCAAGGGCTTCGTCGCCCCTCAGCGGCCCGTGT 244
                                                                                                                                                                                                                                                                          101 ATGTCACGAACGACTGCTCCAACTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGC 160
                                                                                                                                                                                                                                                                                                                                                              ACACCCCCGGGTGCGTGCCTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGC 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 ACACGCAGCTGTACCTGGCCCTGTACGGCGACGACGACGACGCTGATCCTCCTCG 184
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(bases 1 to 526)
Wilson,I., Beswick,R., Shepherd,S., Barker,G., Parker,J., Owen,P., Bakards,D., Coghill,J., Holdsworth,M., Lenton,J., Shewry,P. and
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Contact: Barker G
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic_DNA library"
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Long Ashton, Bristol BS41 9AF United Kingdom.
Location/Qualifiers
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57.5%; Pred. No. 15;
tive 0; Mismatches 54;
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/organism="Triticum aestivum"
                                                                                                       8.5%; Score 40.8; I
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                                                                                                                                                 Matches 129; Conservative
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/mol_type="mRNA"
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/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptI SK', Site_1: BcoRI; Site_2:
Xho1; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
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                                                                                            The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Kaussa DNR Research Institute
Yana 1512-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Chlamydomonas reinhardtii
Bukaryota; Viridiplantes; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Obyama,K.,
Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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/strain="C9"
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Contact: Brika Asamizu
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/strain="cg"
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/clone="Hc074a01_r"
/clone=lhe"Rchlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK; Site_1: BcoXI; Site_2:
/hol; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
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Kazusa DNA Research Institute
Yana 1532-3, Kisazazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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I (bases I to 440)
Asamizu, B., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
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in a medium with bubbling air containing 5% carbon
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Kazusa DNA Research Institute
Yana 1532-3, Kiearazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
    118 CTTCGACCCCCTGGACGCTCGTCGTCGTCGACTTCGCCGTGGGCACCATCTT 237
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Chlamydomonadaceae; Chlamydomonas.
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Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
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ve 0; Mismatches 88; Indels
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/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
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/clone="HC070g06_r"
/clone_lib="Chlamydomonas reinhardtii 5* CO2"
/clone_lib="Chlamydomonas reinhardtii 5* CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed_from cells cultured
in a medium with bubbling air containing 5* carbon
dioxide"
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Masmiru, B., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonadaceae; Chlamydomonas.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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6: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-470-426B-14

US-09-014-416-4

US-09-014-416-6

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US-08-612-973-7

US-08-612-973-7

US-08-487-231-30

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US-08-487-231-30

US-08-827-597-3

US-08-812-973-5

US-08-927-597-5

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28 417.2 86.9 636 3 US-08-927-597-13 Sequence 13, Appl 29 416.8 86.8 742 1 US-08-081-072-18 Sequence 18, Appl 31 416.8 86.8 742 1 US-08-449-093A-18 Sequence 18, Appl 32 416.8 86.8 932 1 US-08-449-093A-15 Sequence 18, Appl 32 416.8 86.8 932 1 US-08-649-093A-15 Sequence 18, Appl 33 415.4 86.5 2116 3 US-08-499-093A-15 Sequence 21, Appl 34 413.8 86.2 501 2 US-08-499-093A-15 Sequence 21, Appl 36 413.8 86.2 501 2 US-07-965-28-28 Sequence 28, Appl 36 413.8 86.2 501 2 US-07-965-28-28 Sequence 28, Appl 36 413.8 86.2 501 2 US-09-201-912-28 Sequence 28, Appl 36 413.8 86.2 11076 4 US-09-201-912-28 Sequence 28, Appl 413.6 86.2 11076 4 US-09-539-601-1 Sequence 1, Appl 413.6 86.2 11076 4 US-09-539-601-1 Sequence 25, Appl 42 405.2 84.4 1167 1 US-08-324-977-9 Sequence 9, Appl 44 405.2 84.4 1167 2 US-08-384-616-9 Sequence 9, Appl 44 405.2 84.4 1167 2 US-08-304-977-9 Sequence 9, Appl 44 405.2 84.4 1167 3 US-08-316-99 Sequence 9, Appl 54 405.2 84.4 1167 3 US-08-316-86-9 Sequence 9, Appl 55 405.2 84.4 1167 3 US-08-316-86-9
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US-08-612-973-11

Sequence 11, Application US/08612973

Patent No. 6150134

GENERAL THFORMATION

APPLICANT MARCTENS GERT
APPLICANT BOSMAN, FONS

APPLICANT BOSMAN FONS

APPLICANT BOSMAN FONS

APPLICANT BOSMAN FONS

APPLICANT APPLICANTON

COUNTRY ALINGTON

CITY: ALINGTON

CONTRY: ALINGTON

CONTRY APPLICANTON

COMPUTER INP PROME PROBABLE FORM:

MEDIUM TYPE: PLOPPY disk

COMPUTER INP PROME PROBABLE

MEDIUM TYPE: PLOPPY DISK

COMPUTER TRADBLE FORM:

MEDIUM TYPE: PLOPPY DISK

COMPUTER THORATION

APPLICANTON NUMBER: 132,020

APPLICANTON MANER: 132,020

APPLICANTON NUMBER: 132,020

TELECOMMUNE (703) 816-400

TELECOM
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241 AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGCTTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCC 360
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Patent No. 6150134

GENERAL INFORMATIONS, GEERT
APPLICANT: MARRIENS
APPLICANT: BOSMAN, FONS
APPLICANT: BUSEN, MARIE-ANGE
APPLICANT: BUSEN, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
CORRESPONDENCE ADDRESS:
ADDRESSE: ALXON & VANDERHYR P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 480; DB 3; Length 480; 100.0%; Pred. No. 4.1e-127; ive 0; Mismatches 0; Indels
     REFERENCE/DOCKET NUMBER: 1487-10
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                         Matches 480; Conservative
                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                   MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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Best Local Similarity
                                                                                                                                                                                                  ANTI-SENSE: NO PEATURE:
                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
FRATURE:
                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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                                                                                                                  1 ATGTCCGGTTGCTCTTTCTCTTCTTCTCTTGGCCCTGCTGTCCTGTCTGACCATACCA 60
                                                                                                                                                                                                                                                        241 AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGGTTTGCTCGTTGGGCT
                                                                                               1 ATGTCCGGTTGCTCTTTCTCTATCTTCGCCCTGCTGTCCTGTCTGACCATACCA
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Sequence 11, Application US/08927597

Sequence 11, Application US/08927597

GENERAL INFORMATION:
APPLICANT: BOSMAN, FONS

APPLICANT: BUYER, MARTHOFF, GUY
APPLICANT: BUYER, MARTHOFF, GUY
APPLICANT: BUYER, MARTE-ANGE
ITILE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
ITILE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
CORRESPONDENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSER: NIXON & VANDRHYUR P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                     Gaps
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                                    Length 480;
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STATE: VIRGINIA
COUNTR: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/927,597
                                                                  0; Indels
                                 Score 480; DB 3; L
Pred. No. 4.1e-127;
                   100.0%; Scc... 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                                                  Matches 480; Conservative
                                                  Similarity
US-08-612-973-11
                                                                                                                                                                                                                                   121
                               Query Match
Best Local S
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PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
APPLICATION NUMBER: US 08/612,973
FILLING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOWAS E.
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
                                                                                                                                                                                                                                                                    ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.4%;
Matches 476; Conservative
                                                                                                                                                                                                                                                                                                                                                            ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
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                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL: N
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FEATURE:
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; LOCATION:
US-08-927-597-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATC 420
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                           COUNTRY: U.S. A. A. COUNTRY: U.S. A. COMPUTER READABLE FORDY disk COMPUTER: IBM PC compatible CONTROL CATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION NUMBER: 1487-10
REFERENCE/MONICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRACTERISTICS:
LERNATH: 483 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: STANDEDESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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ARLINGTON
                   VIRGINIA
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FEATURE:
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LOCATION:
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181 TGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCC 240 9 1 ATGCCCGGTTGCTCTTTCTCTTTCTTCTTGGCCCTGCTGTCTGTCTGACCATACCA 1 ANGTOCOGFFIGOROTTTCTTCTTTCTTTGGCCCTGCTCTCTGTCTGACCATACCA 0; Gaps RESULT 4

18-08-927-597-9

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18-08-927 Length 483; Indels COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/927,597 Score 474.2; DB 3; Pred. No. 1.8e-125; 0; Mismatches 3;

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506 TGCCCGGTTGCTCTTTCTCTTTCTCTTTGGCTTTTGCTGTCCTGTTTTGACCATCCCAG 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08470426B; Patent No. 5856458; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Ploppy disk
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Patent No. 5856458
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Okamorto, Hiroaki
APPL
GCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTCCCGGATCTGTTTTCCTTGTTTCC 360
                                                                                                        241 AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCT 300
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-153402
FILING DATE: 1-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wellacher, Robert G.
TELECOMMUNICATION NUMBER: 06/59-47083.1
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1850 M Street, N.W., Suite 800 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
TOPOLOGY: unknown
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-470-426B-17
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APPLICANT: Okamoto, Hiroaki
APPLICANT: Nakamura, Tetsuo
TITLE OP INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
TITLE OP INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
TITLE OF INVENTION: HEPATITIS VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                     685
                                                                                                                                                                                   241
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566 CTTCCGCTTATGAAGFGCGCAACGTGTCCGGGATATACCATGTCACGAACGACTGCTCCA 625
                                                                                                                                                                                                                                                                                                        242 GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 AGCTGTTCACCTTCTCACCTCGCCGCATCAAACAGTACAGGACTGCAACTGCTCAATCT 421
                                                                                           686 GCGTTCGGGAGGACAACAGCTCCGTTGCTGGGGTAGGGTCACTCCCACGCGCGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           866 AGCTGTTCACCTTCTCGCCTCGCCTGGATGAGACAGTGCAGGACTGCAACTCT
                                                       182 GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
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ADDRESSEE: L.L.P.
STREET: 1850 M Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTRARE: Patentin Release #1.0, Version #1.30
SOFTRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-153402
PILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/59-47083.1
TELEBPHONE: (202) 655-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELBFAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1863 base pairs
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TYPE: nucleic acid
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GENERAL INFORMATION:
APPLICANT: Yanagi, Masayuki
APPLICANT: Yanagi, Masayuki
APPLICANT: Yanagi, Masayuki
APPLICANT: Bubth, Jonas
APPLICANT: Bubth, Jonas
APPLICANT: Breadil, Robert H.
TITLE OF INVENTION: CLORED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
TITLE OF INVENTION: USES THERBOF
TITLE OF INVENTION UNBERE: US/09/014,416
CURRENT APPLICATION NUBBER: US 60/053,062
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN VOF: 2.1
SEQ ID NO 6
                                                                                                                                                                                                        1027 GTGTTCAGGAGGGTAACAGCTCCCGTTGCTGGGTAGCGCTCACTCCCCACGCTCGCGCGCCA 1086
                                                                                                                                                                                                                                                                             1147 CTGCTTTCTGCTCCGCTATGTACGTGGGGGATCTCTGGGGGATCTATTTTCCTCGTCTCCC 1206
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                        182 GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                  362 AGCTGTTCACCTTCTCACCTCGCCGCATCAAACAGTACAGGACTGCAACTGCTCAATCT
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Pred. No. 5.9e-112;
0; Mismatches 30; Indels
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US-09-014-416-6
Sequence 6, Application US/09014416
Patent No. 6153421
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Best Local Similarity 93.7%;
Matches 446; Conservative
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; ORGANISM: Hepatitis C virus
US-09-014-416-6
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APPLICANT: Bukh, Jens
APPLICANT: Bukh, Jens
APPLICANT: Bukh, Jens
APPLICANT: Emerson, Susanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
FITLE OF INVENTION: USES THERROF
FILLS REFERENCE: 20264276
CURRENT APPLICATION NUMBER: US/09/014,416
CURRENT APPLICATION NUMBER: US 60/053,062
EARLIER PILING DATE: 1999-01-27
EARLIER FILLING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
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                                                                                                                                                                     2 TGTCCGGTTGCTCTTTCTTTCCTCTTGGCCCTGCTGTCTGTCTGACCATACCAG
                                                                                                                                                                                                                                                   182 GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTCGCGGCCA
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                                                                                                                                    Gaps
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                                                                                             Length 1863;
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                                                                                                                                Indels
                                                                                           Score 431.2; DB 2;
Pred. No. 4.4e-113;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09014416
Patent No. 6153421
GENERAL INFORMATION:
                ; TOPOLOGY: unknown; MOLECULE TYPE: DNA (genomic)
US-08-470-426B-14
                                                                                           Query Match
Best Local Similarity 94.1%;
Matches 448; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
  single
STRANDEDNESS:
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                                                                                                               242 GGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCTG 301
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                                                                            275 ACTCAAGCATTGTGTATGAGGCGGGCGTGATGATGATGACACCCCCGGGTGCTGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08927597

Parent No. 6245503

GENERAL INFORMATION:
APPLICANT: MAGRIENS, GERT
APPLICANT: BOSWAN, FONS
APPLICANT: BUYSE, MARIB-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSER: NIXON & VANDERHYR P.C.
STREET: 1100 NORTH GLEBB ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUMTRY: U.S.A.
ZIP: 22201-4714
COMPUTER RABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BYRNE, THOMAS E. REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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CIGCITTCIGCICCGCTAIGHAGTACGTGGGGGATCTCIGCGGATCTATTTCCTCGTCTCCC 1206
                                                                                                                                                                        CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCC 361
                                                                                                                                                  AGCTGTTCACCTTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTAATCT 421
                                                                                                                                                                                                                                            ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTAA 477
                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MARRYENS, GERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUYES, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.8%; Score 426.2; DB 3;
93.1%; Pred. No. 8.4e-112;
iive 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION: 435
NAME: BYRNE, THOMBATION:
NAME: BYRNE, THOMBER 32,205
REGISTRATION NUMBER: 1487-10
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ 1D NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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HYPOTHETICAL:
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LOCATION:
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LOCATION:
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US-08-612-973-7
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RESULT 12
US-07-965-285-30
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APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Forchon, Colette
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Applications
TITLE OF INVENTION: Applications
NUMBER OP SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                              274
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                                                                                                                                                                                                                                        Length 633;
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                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                          Score 426.2; DB 3;
Pred. No. 8.4e-112;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/08483695; Patent No. 5866139; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                        88.8%;
SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOCHETICAL: NO
ANTI-SERNE: NO
FEATURE:
                                                                                                                                                                                                                                                                       Matches 446; Conservative
                                                                                                                                                                                 mat_peptide
                                                                                                                                                  1..630
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                               , LOCATION:
US-08-927-597-7
                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopyy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWAREN APPLICATION DATA:
APPLICATION NUMBER: US/08/483,695
FILING DATE:
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR-1993
APPLICATION NUMBER: RR 91 06 882
FILING DATE: 06-JUN-1991
ATORNEY/AGENT INFORMATION:
NAME: MAYERS (SEGUEL)
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 05284000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 423.4; DB 2;
Pred. No. 4.9e-111;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: Other
DESCRIPTION: cDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/07965285; Patent No. 5879904; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.4
Matches 439; Conservative
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APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Notlocide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
397 AGCTGTTCACCTTCTCGCCTCGCCGGCATGAGACAGTGCAGGACTGCAACTGCTCAATCT 456
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                                                                                                         422 ATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGA 466
                                                                                                                                                                     457 Arcccccarrrarcacercacccarecerrecararcarea 501
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,231
FILING DATE: 07-JUNE-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/965,285
FILING DATE: US 085
FILING DATE: US 07/965,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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Pred. No. 4.9e-111;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 05,286-0001-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Other DESCRIPTION: cDNA to genomic RNA
                                                                                                                                                                                                                                                                                                    US-08-487-231-30
; Sequence 30, Application US/08487231
Patent No. 5919454
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.2%;
Best Local Similarity 94.4%;
Matches 439; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202-408-4400
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STRANDEDNESS: single
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                        APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OP SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
ADDRESSE: Dunner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 GCGTTCGGGAGACAACAGCTCCCGTTGCTGGGTAGCGCTCACCCCACGCTCGCGCGCA 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 GGAATGCCAGGCTCCCCACTACGACAATACGACGCCCACGTCGACTTGCTCGTTGGGCGG 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR-1993
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 06 882
FILING APPLICATION NUMBER: FR 91 06 882
FILING APPLICATION NUMBER: PR 91 06 882
RIENG BATE: 06-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS KENNELD:
REGISTERATION NUMBER: 55,146
REFERENCE/DOCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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94.4%; Pred. No. 4.9e-111;
ive 0; Mismatches 26;
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   Christian
                                                                                                                                                                                                                                                                                                                                    STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 88.2%;
Best Local Similarity 94.4%;
Matches 439; Conservative
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202-408-4400
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Brechot,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-965-285-30
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 91-9510
FILING DATE: 10-JUN-1991
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CORRESPONDENCE ADDRESS:
             Query Match
Best Local Similarity 94.4%;
Matches 439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: YANG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Daejeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Daejeon
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LEE,
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APPLICANT: Brechot, Christian
APPLICANT: Brechoff, Una
APPLICANT: KremsGorf, Una
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Applications
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                     397 AGCTGTTCACCTTCTCGCCTCGCCGCATGAGACAGTGCAGGACTGCAACTGCTCAATCT 456
                                                                  241
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                                                                                                                                 CTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTTGTTTCCC 361
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217 CCGTTCGGGAGGACAACAGCTCCCGTTGCTTGGGTAGCGCTCACTCCCACGCTCGCGGGCCA
                                                                  182 GCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGGGGCGCTCACTCCCACGCTCGCGGCCA
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ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 05286-0001-00000
REFERENCE FOOKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: cDNA to genomic RNA
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,285
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 30, Application US/09201912; Patent No. 6210962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INPORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-201-912-30
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 Length 501;
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Score 423.4; DB 3;
Pred. No. 4.9e-111;
0; Mismatches 26;
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APPLICATION NUMBER: US/08/150,204E
FILING DATE: 20-Apr-1994
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jae Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Republic of Korea ZIP: 305-340
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 96, Application US/08150204E Patent No. 6538126 GENERAL INFORMATION:
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LIM, Kook Jin
CHOI, Deog Young
SO, Hong Seob
KIM, Chun Hyung
KIM, Sung Taek
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Jae Young
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                                                                                                                                                                                                                                                    CTHER INFORMATION: KHCV-LBC1, Fig. 2 SEQUENCE DESCRIPTION: SEQ ID NO: 96 US-08-150-204E-96
APPLICATION NUMBER: KR 91-13601
PILING DATE: 6-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam, Esq.
REGISTRATION NUMBER: 32,507
REGISTRATION NUMBER: 32,507
REPERENCE/DOCKET NUMBER: 2695/FLK
TELECOMMUNICATION INFORMATION:
TELEFONE: (212) 940-8564
INFORMATION FOR SEQ ID NO: 96
SEQUENCE CHARACTERISTICS:
LENGTH: 9472 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: INFO: DARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Search completed: June 16, 2004, 13:30:24 Job time : 35.6 sece